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Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
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gge tea etg ege ace tae eea tgg ggt tea aga aca etg ate get gat Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp 10 15

											gaa Glu 35			211
		_									aac Asn	-		259
											acg Thr			307
_	_		_								atc Ile		_	355
											gaa Glu			403
_	_		_	_	_		_			_	ctc Leu 115		_	451
_		_		_	_						ctg Leu		_	499
											ctg Leu			547
				_	_	_	_	-			gac Asp	-		595
											cgc Arg			643
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Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro 20 25 30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu 165 170 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys 180 185 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu 195 200 205

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							cgt Arg 40									144
							gtc Val									192
_	_	_	_	-		-	cca Pro					-	_			240
							cgt Arg									288
_	_	_	_	_		_	cgt Arg	_	_	_	_					336
							ggt Gly 120									384
							act Thr									432
							tac Tyr									480
-	-		_	_		_	aat Asn		_	_		_	_			528
_			_	_		-	att Ile				_				_	576
-	_		_		_		acc Thr 200		-	-		_		_	_	624
							ttg Leu									672
							tgg Trp							Phe		720
							att Ile									768

	245		250	255	
			ttt gat aat ga Phe Asp Asn As		-
_	Glu Val Tyr		aag ttc tgg gt Lys Phe Trp Va 28	al Asp Leu	
		-	cac act aag co His Thr Lys Pr 300	_	
		-	aaa tca aac co Lys Ser Asn Pr 315		
			gca cgt ctg ta Ala Arg Leu Ty 330	_	
	_		tac ttc acc to Tyr Phe Thr Tr		
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	-		gta tat tcc go Val Tyr Ser GJ 410		
			tcg gaa gag ta Ser Glu Glu Ty		
	Glu Leu Arg		ttc gag ggt gc Phe Glu Gly Al	a Leu Glu	
		_	ctg ctc aac ca Leu Leu Asn Gl 460	_	-
			aac atc cac tt Asn Ile His Ph 475	_	
			aag gtt gat go Lys Val Asp Al 490		

aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu 500 505 510	1536
gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala 515 520 525	1584
cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser 530 535 540	1632
gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile 545 550 555 560	1680
ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp 565 570 575	1728
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465

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Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu 500 505 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser 530 535 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile 550 555 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp 565 570 Arg Glu Ile Lys Thr Tyr Arg Ala 580 <210> 361 <211> 2316 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2293) <223> RXA02612 <400> 361 gaacttccag cgtctcgccg tgagcgtctc gcgtggcgcg aaatcaagac ctaccgcgcg 60 taatttccca tctctgtacc ttctatcaag gattatcatc atg acc gtt gac ccc 115 Met Thr Val Asp Pro gcg age cae ate ace ate cet gaa gea gat etg gee ege etg ege cae 163 Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His 10 tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa 211 Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu 25 get ggt teg gtt ate ege aeg ege eag gte gge geg aeg eag gtt aat 259 Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn 40 45 ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac 307 Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp 55 60 att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355 Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu 70 gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac 403

Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr

90 95 100 tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu 105 gga cgc cat gag cgt ttg tgg gag att ctc ggt gcc aac atc aag acc 499 Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly Ala Asn Ile Lys Thr tac caa act gcg ctc gga aca gtt cgt ggc acc gca ttt act gtg tgg 547 Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr Ala Phe Thr Val Trp 135 gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg 595 Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Phe Asn Gly Trp 150 155 aat gca tcc cag cat ccg atg cgt tct atg ggt ggt tcg ggt ctg tgg 643 Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp 170 gag ctg ttc atc cca ggc ata gag gaa ggc gaa gtg tac aaa ttc gcc 691 Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala 185 gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct 739 Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala 200 cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct 787 Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser 215 gag tac cag tgg cag gat tcc gag tgg ctg cgc gag cgt tcc caa act 835 Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr 230 gat etc gea tec aag eea atg agt gte tae gag gte eac etc ggt tet 883 Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser 250 tgg cgc tgg ggt aag aac tat gag gat ttg gct act gag ctg gtt gat 931 Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp 265 270 tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca 979 Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala 285 gag cac ccc ttc ggt ggt tcc tgg ggt tac cag gtc acc ggc tac tac 1027 Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln Val Thr Gly Tyr Tyr 300 gca ccg acc tct cgt tgg ggt act cca gat cag ttc cgt gcg cta qtc 1075 Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val gac gct ttc cac gcc cgc ggt att ggc gtg atc atg gac tgg gtt cct 1123 Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile Met Asp Trp Val Pro 335

gcc Ala													1171
gcc Ala													1219
ggc (													1267
gtc Val 390	_		_			_	_			_		_	1315
cgc (				_	_	_			_		_		1363
cac (													1411
gca Ala											-		1459
cct Pro													1507
acc Thr 2 470													1555
atg (				_									1603
cac His													1651
ttc Phe													1699
ggc (													1747
gcc d Ala 2 550	_		_					_					1795
aag i Lys :													1843

					cca Pro										1891
		-			cgc Arg		_							_	1939
	_				ctg Leu 620			_	_				_		1987
			_		gac Asp	-	-					_			2035
			_	_	ggc Gly		_	_	_	_	_			_	2083
			_		gag Glu		_			_	_	_			2131
_	 _		_		aac Asn		_	_	_	_				_	2179
_	_		_		tcc Ser 700	_		-	-				_	-	2227
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Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly 35 40 45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr 50 60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg 65 70 75 80

Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile 105 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly 115 120 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr 135 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly 170 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys 200 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser 215 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln 295 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala 345 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu 375 380

Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe

395

400

His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly 425 Arg Glu Asn Leu Glu Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr 455 Ser Trp Pro Gly Val Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe 485 Ser Lys Asn Pro Val His Arg Ala Phe His His Ser Glu Leu Thr Phe 505 Ser Leu Val Tyr Ala Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met 545 555 Trp Ser His Pro Gly Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp 615 Phe Thr Gly Glu Gly Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala

Ala Thr Pro Arg Asp Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro

710

Ala Met Ser Ala Gln Phe Tyr Ser Leu Gln Lys

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				cta Leu											96
				ccc Pro											144
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				att Ile			_					-			240
				ccc Pro 85											288
				gtt Val											336
				tcc Ser			_	_	_	-		-	_	_	384
				ctg Leu											432
				ctt Leu											480
				acc Thr 165											528
				ctc Leu											576

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											gat Asp					720
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					_	_	-	_			gag Glu	-			_	816
-			-	_			-		_		cac His		_			864
	_		_	_					_		gag Glu 300		_	_	_	912
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											ctg Leu					1056
											agc Ser					1104
											agg Arg 380					1152
											gac Asp					1200
											gat Asp					1248
											ggc Gly					1296

gag cct gat tat cga Glu Pro Asp Tyr Arc 435		Ile His Asp		
atg ttc aac gct cad Met Phe Asn Ala His 450	-	-		
cat ttc ggt atg aag His Phe Gly Met Ly: 465			-	
ggc cac ccg ctg gag Gly His Pro Leu Glu 489	Asp Leu Thr			
gtt cct gcc cgt tcc Val Pro Ala Arg Sec 500				
tac acc aag ctt gag Tyr Thr Lys Leu Glu 515	· -	Ala Ala Glu		<u>-</u>
ctt gcg gca gag aag Leu Ala Ala Glu Lys 530				
gca gca aag gaa gc Ala Ala Lys Glu Ala 545				
gaa cgt gct tcg act Glu Arg Ala Ser Th 569	Gln Glu Ala			
gat gcg att gcc ga Asp Ala Ile Ala Asp 580				
gat gaa gta gcg gca Asp Glu Val Ala Ala 595		Thr Glu Pro		
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330

Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn 340 345 350

Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg 355 360 365

Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Gln Phe 370 375 380

Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala 385 390 395 400

Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe 405 410 415

Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu 420 425 430

Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu 435 440 445

Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu 450 455 460

His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val 465 470 475 480

Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr 485 490 495

Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp 500 505 510

Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu 515 520 525

Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala 530 535 540

Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala 545 550 555 560

Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala 565 570 575

Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln 580 585 590

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ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg

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_				_	_	-	_		_	gca Ala 235				_		720
										ttg Leu						768
-	_	-		-		-	_			gga Gly		-	_			816
										ctg Leu						864
	_	-		-			_		_	gga Gly	_				_	912
										ttc Phe 315						960
								_	_	tgg Trp	_		_	_	_	1008
										gat Asp						1056
							-	_		acg Thr	_	_	_	_	_	1104
							_			gaa Glu	_		_	_	_	1152
										gaa Glu 395						1200
										gaa Glu						1248
										cag Gln						1296
										gag Glu						1344
										gag Glu						1392

450 455 460

gac acc gag cct gac act gaa tct gac tcc gag cag gct gag gta gct
Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala
465 470 475 480

tca gag gag cct gaa gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt 1493 Ser Glu Glu Pro Glu Ala Asp Glu Glu Glu Lys 485 490

cgc 1496

<210> 366

<211> 491

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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1 5 10 15

Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln 20 25 30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp 35 40 45

Val Gly Glu Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr 50 55 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly 65 70 75 80

Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser 85 90 95

Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe 100 105 110

Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn 115 120 125

Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser 130 135 140

His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro 145 150 155 160

Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr 165 170 175

Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met 180 185 190

Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu
195 200 205

Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val 210 215 220

Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe 225 230 235 Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg 245 Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn 280 Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe 315 Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala 345 Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu 375 Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg

Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala
420 425 430

His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro

Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Gļu Asp Ala Ala Glu Ala

Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro 450 455 460

Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala 465 470 475 480

Ser Glu Glu Pro Glu Ala Asp Glu Glu Lys 485 490

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<211> 547

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> RXA01111

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<213> Corynebacterium glutamicum

<400> 368

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Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp 40

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp

50 55 60 His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp 105 Gly His Pro Ser Leu Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro 115 120 Asn Gly Arg Asn Thr Glu Asp Ser Ile Asp His Thr Met Lys Ser Val 135 Val Val Asn Pro Phe 145 <210> 369 <211> 1635 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1612) <223> RXN01550 <400> 369 ttcgccagca gtacttcttc acctctgctt ccctgcaggc catgattcag ggccacctgg 60 cgcaccacaa ggacctcagc aactttgccg agttcactcc gtg cag ctc aat gac 115 Val Gln Leu Asn Asp 1 act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac 163 Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp 10 gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc 211 Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr tto goa tac acc aac cac acc gtg ctc acc gaa get ett gag cag tgg 259 Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp 40 45 gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tqg gaa atc atc 307 Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg 355 Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt 403 Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val 95

				att Ile												451
				acc Thr				_	_			_	_	_		499
	-	_		cca Pro		-				_				_		547
				ctg Leu		_								_		595
				ggt Gly 170												643
				tcc Ser												691
				gct Ala												739
	_	_		att Ile			_		_				-		_	787
	_	_		cac His			_	_	_		_					835
_		_		tac Tyr 250		_		_	_	_				-		883
				gtc Val												931
			-	att Ile		_						_		_	-	979
		_		gag Glu	-		_	_		_		_		_		1027
			_	tcc Ser		_				_				_	_	1075
				tcc Ser 330												1123

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_	_		_	_		ggc Gly	_			_			_	_		1171
						gat Asp										1219
		_	_		_	gaa Glu 380	_		_	_		_	_			1267
						acc Thr	-				_	_	-	-	-	1315
						ctc Leu										1363
_		_			_	atc Ile						-	_	_	-	1411
						gat Asp		_	_		_			_	-	1459
_			_	-		gcc Ala 460		_		_			_	_	_	1507
-					-	gag Glu			_				_	_		1555
	_	_		-		gag Glu			_						-	1603
	aag Lys		tago	gtttļ	caa d	cctco	egett	ic ta	aa							1635

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<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

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Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg

50 55 60 · Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr 105 Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly 155 Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser 185 Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser 215 Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu 315 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala 325 Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu 345 Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu 355 360 Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu 375 380

Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu 385 395 Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn 410 Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly 420 425 Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu 455 Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys 500 <210> 371 <211> 1367 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1344) <223> FRXA01550 <400> 371 atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc aca gag atc 48 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag 96 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu 20 acc atc gac egc atg get eca atc eag egc act gtt eat atg gea 144 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala 35 tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg 192 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu 50 cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg 240 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu 65 70 tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt 288 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg 85 90 95

tgg ( Trp 1	_	_	_					_		_	_			_		336
tcc (			_	_		_		_	_	_		_	-	_	_	384
cgc f																432
aag d Lys 1 145	_	_		-		_		_						_	_	480
ggc a				-		-				-		_		_	-	528
ctc (		_		_	_	_		_					_		_	576
ctt i Leu '																624
act of Thr																672
gcg Ala 225																720
cct (		_		_	_		_		-		-					768
gtc :																816
att : Ile :			_		_	-	_	_					_	_		864
atg a Met 1	_			_			_			_	_		_		_	912
gag Glu 305																960
cgc ( Arg '		_	_	_		_	_	-	_	_						1008
ctc	tat	gag	acc	gtc	cct	ggc	ctc	aag	cgc	gca	ttg	gac	gcc	ctg	gat	1056

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340 345 350	Asp													
aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu 355 360 365	•													
cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr 370 375 380														
gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met 385 390 395	_													
gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp 405 410 415														
aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg 420 425 430														
tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys 435 440 445														
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Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu														
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu151015 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu	Glu													
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu151015Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu 2530Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met	Glu Ala													
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu 101015Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu 202530Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met 4045Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala	Glu Ala Leu													
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu 10101115Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu 2025252530Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met 4045Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala 505560His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala	Glu Ala Leu Leu 80													
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu 1011115Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu 2025Ala Asp Gly Leu Asp Glu 30Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met 4045Ala Ala Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Ala 50Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Ala 55Ala Glu Thr Leu Ala Asp Trp Tyr Ala 75Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg	Glu Ala Leu Leu 80 Arg													
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu 1010Ile Thr Glu 15Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu 2025Ala Asp Gly Leu Asp Glu 30Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met 4040Ala Asp Gly Val Ala Ala Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Ala 50Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Ala 505560His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala 75Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg 8590Yal Thr Pro Arg 95Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg	Glu Ala Leu BO Arg Leu													

130 135 140 Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln 150 Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg 165 Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp 185 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asp 230 235 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu 330 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys 360 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala 390 395 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile 405 410 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp 425 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys 435 440

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gca Ala	ttc Phe	tgc Cys 195	gaa Glu	gct Ala	cgt Arg	ggt Gly	ctg Leu 200	aag Lys	cgc Arg	tca Ser	tct Ser	gtt Val 205	gca Ala	cac His	ctc Leu	624
						ttc Phe 215										672
	_			_		tac Tyr		-	-			_	-	_		720
						cac His			-		_			-	_	768
						cgt Arg										816
						ggt Gly										864
						cac His 295										912
						aat Asn										960
_	_	-	_		-	ggc Gly	-			-						1008
					_	acc Thr			-		_	_	_		-	1056
_			_	-		ctc Leu		_	_	_						1104
						tgg Trp 375										1152
						aac Asn										1200
						aag Lys										1248
						tcc Ser										1296
att	ggt	ttc	gca	cgt	cgc	gta	tcc	acc	tac	aag	cgc	ttg	acc	ttg	atg	1344

Ile	Gly	Phe 435	Ala	Arg	Arg	Val	Ser 440	Thr	Tyr	Lys	Arg	Leu 445	Thr	Leu	Met	
	cgc Arg 450															1392
	gtt Val															1440
	aag Lys															1488
-	cgt Arg	_	_				_		_		_			_	_	1536
_	tac Tyr	_				_	_			_					_	1584
	cag Gln 530															1632
	ctg Leu						-				-	_	_		_	1680
	acc Thr								-			_	_	_	_	1728
	cgc Arg	-		-	-		_		_		_	_	-	-		1776
	gtt Val			Leu	Phe	Tyr		Arg	Asp	Lys	Asn					1824
	tgg Trp 610															1872
	acc Thr															1920
	acc Thr															1968
	tac Tyr															2016
	gtc Val															2064

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Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly 485 490 495

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Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg 515 520 525

Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly 530 535 540

Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys 545 550 555 560

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565 570 575

Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn 580 585 590

Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
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Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg 625 630 635 640

Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala 645 650 655

Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val 660 665 670

Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu 675 680 685

Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu 690 695 700

Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile 705 710 715 720

Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr 725 730 735

Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala 740 745 750

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200

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	gac Asp	_								_	_	_	_			864
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Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met 50 60

Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu 65 70 75 80

Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
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Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala 100 105 110

Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro 115 120 125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg 130 135 140 IleProLeuLeuLeuAspThrAsnIleGluAlaAsnProGluGlu145IleArgAsnValThrAspArgLeuTyrGlyGlyAspAsnGluHisArg165Ile

Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu 195 200 205

Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220

Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240

Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255

Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gln Pro Glu 260 265 270

Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285

Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300

Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
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Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val  $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350$ 

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tat cg															451
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ggt ggc att Gly Gly Ile									883
gcg tat cag Ala Tyr Gln				Pro Arc					931
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Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn 130 135 140

Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr 145 150 155 160

Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala 165 170 175

Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile 180 185 190

Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val 195 200 205

Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu 210 215 220

Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly 225 230 235 240

Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser 245 250 255

Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg 260 265 270

Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu 275 280 285

Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val 290 295 300

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115

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Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp

100 105 110 Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp 120 Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro 135 Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu 185 Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro 200 Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp 215 Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu 235 Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg 330 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val 345 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu 370 375 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn 395 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln 405 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly 420 425

Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp 435 Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe 455 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val Asp Ala Ser Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Glu Leu Leu 500 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val 535 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu 565 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg 610 <210> 383 <211> 658 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(658) <223> RXA01888 <400> 383 agtagatact agataccacc cattgatgcc gtcaaggggt ttcctgtaaa gatgtaagag 60 attaagaaaa gaggtagata tggcgtcaaa gcgaccgaca atg gct gat gtg gca 115 Met Ala Asp Val Ala 1 aaa get get gga gta tee aet geg etg gte tee ate gtg ttt ege gat 163 Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp 10 15 20 gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala

			25					30					35			
_	_				att Ile		_	_	_	_				_		259
					atc Ile											307
					gaa Glu 75											355
	_	_			agc Ser				_		_		-		_	403
					atc Ile											451
					cct Pro											499
					gcc Ala											547
_		_	_		gca Ala 155	-		-			_					595
					gaa Glu						-			-	-	643
			cag Gln 185	_												658
<211 <212	0> 38 l> 18 2> PE 3> Co	36 RT	ebact	ceriu	um gl	Lutar	nicur	n								
	)> 38 Ala		Val	Ala 5	Lys	Ala	Ala	Gly	Val 10	Ser	Thr	Ala	Leu	Val 15	Ser	
Ile	Val	Phe	Arg 20	Asp	Ala	Pro	Gly	Ala 25	Ser	Glu	Ser	Thr	Arg 30	Asn	His	
Val	Lys	Glu 35	Lys	Ala	Ala	Glu	Leu 40	Gly	Tyr	Ile	Pro	Asp 45	Arg	Arg	Ala	
Gln	Lys 50	Leu	Arg	Gln	Asn	Arg 55	Ser	Gly	Leu	Ile	Gly 60	Val	Ala	Phe	Glu	

Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr 85 Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu 105 Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr 115 120 125 Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu 150 155 Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile 170 Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu 180 <210> 385 <211> 1503 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1480) <223> RXN01927 <400> 385 gagcagcggg atcttttgcg taattcgcgc gcgcagatcc atgtgattga ccacaatggt 60 gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt 115 Met Ala Leu Val Leu gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163 Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala 10 gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211 Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly 30 tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc 259 Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr 45 gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307 Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln 60 cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala 70 75 80

										gct Ala						403
-					_		_			gat Asp				_		451
	-	_				-			_	cgg Arg		-	_	_		499
_		_		-		_	_		_	gtg Val	_	_			-	547
										cgc Arg 160						595
										acg Thr						643
										cat His						691
										aca Thr						739
		-	-		_		_		-	gcg Ala	_					787
						-	-			atc Ile 240					-	835
_		_		_			_	_		gat Asp				_	-	883
										ttc Phe						931
										cgc Arg						979
_		-			-			_	_	gct Ala	_					1027
										ggc Gly 320						1075

cgt cArg in a cgc a Arg in a cgc a	gag Glu gat Asp atc Ile 375	Ala gac Asp gct Ala 360 cag Gln cct	Ala ttt Phe 345 gta Val	Arg 330 gcc Ala acg Thr	cga Arg gcg Ala	Val gca Ala ctg	act Thr gtt Val	Ala gtt Val 350	Gly 335 gaa	Leu ggc	Asn ttg	Cys	Ala ttg Leu	Thr 340 gca	Thr	1123
gat of Asp A cgc a Arg 1	gat Asp atc Ile 375	gct Ala 360 cag Gln	Phe 345 gta Val ctc	Ala acg Thr	Arg gcg Ala ggt	Ala	Thr gtt Val	Val 350					Leu			1171
cgc a Arg 1	atc Ile 375	Ala 360 cag Gln cct	Val ctc	Thr	Ala ggt		Val	gag					355			
Arg 1	Ile 375 gcc	Gln					365									1219
					стх											1267
390		110														1315
gaa t Glu 1																1363
ggt g Gly G																1411
cgc g Arg A																1459
gct g Ala A	_	_	_				taga	agcto	cga t	tatto	gtcga	at ca	ıa			1503
<210><211><211><212><213>	> 46 > PF	0 T	ebact	eriu	ım gl	lutam	nicum	n								
<400>	_		17 m l	T	C1	T1-	7	C	0	m b	C1	0	<b>Q</b>	T	<b>7</b> .1 -	
Met A	нта	Leu	vai	5	GIÀ	iie	Asp	ser	10	Thr	GIN	ser	Cys	15	АІа	
Leu I	Leu	Val	Asp 20	Ala	Ala	Thr	Gly	Gln 25	Val	Ile	Asp	Glu	Gly 30	Arg	Ala	
Ser H	His	Pro 35	Ser	Gly	Ser	Glu	Val 40	Asp	Pro	Arg	Ala	Trp 45	Ile	Ala	Ala	
Leu A	Asp 50	Gln	Ala	Thr	Glu	Gly 55	Leu	Leu	Glu	Arg	Ala 60	Asp	Ala	Val	Ser	
Ile A	Ala	Gly	Gln	Gln	His 70	Gly	Met	Val	Ala	Leu 75	Asp	Glu	Asn	Asp	Glu 80	

Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala

90

95

85

Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
100 105 110

Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg
115 120 125

Trp Met Arg Asp His Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val 130 135 140

Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg 145 . 150 155 160

Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr 165 170 175

Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His
180 185 190

Glu Val Glu Leu Pro Glu Leu Leu Ala Pro As<br/>n Ala Ile Ala Gly Thr $195 \hspace{1.5cm} 200 \hspace{1.5cm} 205$ 

Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala 210 215 220

Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile 225 230 235 240

Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp 245 250 255

Pro Ser Gly Leu Val Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe 260 265 270

Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg 275 280 285

Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala 290 295 300

Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly 305 310 315 320

Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu 325 330 335

Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly 340 345 350

Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr 355 360 365

Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser  $370 \hspace{1cm} 375 \hspace{1cm} 380$ 

Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val 385 390 395 400

Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala 405 410 415

Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro

420 425 430 Gly Ser Asp Pro His Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr 455 <210> 387 <211> 1139 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1116) <223> FRXA01927 <400> 387 aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat gag gag atc 48 Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct 96 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu 35 aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc 192 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr 240 tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala 65 288 tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp 85 cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg 336 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu 100 105 gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct 384 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag 432 Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln 135 cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg 480 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met 150 155 ace gtt caa cat age gte cae gat eea tet ggt ttg gte aet ggt tte 528 BGI-126CP - 558 -

Thr	Val	Gln	His	Ser 165	Val	His	Asp	Pro	Ser 170	Gly	Leu	Val	Thr	Gly 175	Phe	
-	_	-	_			tat Tyr		_	_	_	-	_				576
						ggc Gly										624
						ctg Leu 215										672
		-			-	gag Glu			_	_	_		_		_	720
						gga Gly										768
	_	-	-		-	gaa Glu		_	_	-	_	-	_	_	_	816
						gcc Ala										864
						cgt Arg 295										912
						att Ile										960
			Ala	Ala	Arg	cag Gln	Ala	Ala	Trp	Ala	Leu	Ser	Gly		Ala	1008
						act Thr										1056
						acg Thr										1104
_	ggt Gly 370			taga	agcto	cga t	atto	gtcga	at ca	aa						1139

<sup>&</sup>lt;210> 388

<sup>&</sup>lt;211> 372

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Corynebacterium glutamicum

<400> 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
20 25 30

Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu 35 40 45

Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr 50 60

Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
65 70 75 80

Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp 85 90 95

Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu 100 105 110

Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala 115 . 120 . 125

Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln 130 135 140

Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met 145 150 . 155 160

Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe 165 170 175

Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly 180 185 190

Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu 195 200 205

Glu Phe Asp Ala Leu Ala Leu Ala Gln Pro Gly Ser Gly Gly Val 210 215 220

Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala 225 230 235 240

Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp 245 250 255

Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala 260 265 270

Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln 275 280 285

Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro 290 295 300

Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val 305 310 315 320 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro 340 345 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr 360 Gln Gly Trp Tyr 370 <210> 389 <211> 844 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(844) <223> RXA02729 <400> 389 gaattaattg caggcacggt acctagcgtg acgaaaacta cgatccccac tgcccttatt 60 catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115 Met Asp Ser Pro Met agt aac toa acc ggt acc gac att gtc gtt gtc gga toc atc aat gcc 163 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Gly Ser Ile Asn Ala 10 gat etc ace gea aaa gtt eaa ege eac eet gaa eet gga gaa ace etc 211 Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu ctg ggt agc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259 Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355 Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403 Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly 95 ctt gcc atc atc gtg tct gac gat ggg gaa aac acc atc gtt 451 Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val 105 110 atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499 Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His 120 125

	caa Gln 135				_				_	_				547
	gcc Ala	_			-	-	_	-				-		595
	atc Ile													643
-	gcc Ala	_	-	_	_		_		_	 _	_		_	691
-	atg Met						_		_		_		-	739
	gaa Glu 215													787
-	gaa Glu		 _	_		_	_			_	_			835
	cca Pro	_												844

<210> 390

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly 35 40 45

Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val $50 \\ 55 \\ 60$ 

Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu 65 70 75 80

Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val 85 90 95

Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu 100 105 110

Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu 120 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu 130 135 140 Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu 155 Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly 165 His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu 185 Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val 215 Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln 225 235 Leu Thr Ala Ile Pro Thr Pro Lys 245 <210> 391 <211> 1026 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1003) <223> RXA02797 <400> 391 acagteteat gaageeataa taaceaeett etacaaagat egaegtagaa tggaataaee 60 ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115 Met Asn Asn Arg Ile gte gta gte gge tee ate aac get gat ett aat gtt ete gtt gae ege 163 Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg 10 cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211 His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr 25 gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259 Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Leu Gln Gly 40 45 gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307 Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala 55 60 65

						tcg Ser									355
						ggg Gly									403
-					_	gtc Val							_	-	451
	_	_	_	_	_	caa Gln 125		-			_	_	_		499
						atc Ile									547
			-		_	gtc Val							_		595
						ctt Leu									643
						ctg Leu									691
						gcg Ala 205		_			_	_			739
						gga Gly									787
						gcc Ala									835
						ttt Phe									883
						gac Asp									931
						gcc Ala 285									979
					tct Ser 300	gtt Val	taaa	aaaa	act a	attta	aagaa	ag ag	gg		1026

<210> 392

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Asn Asn Arg Ile Val Val Gly Ser Ile Asn Ala Asp Leu Asn 1 5 10 15

Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
20 25 30

Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala 35 40 45

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
50 55 60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val 65 70 75 80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val 85 90 95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
100 105 110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu 115 120 125

Leu Ala Glu Ala Gly Ile Leu Leu Gln Gly Glu Ile Pro Ala Asp 130 135 140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn 145 150 155 160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp 165 170 175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe 180 185 190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu 195 200 205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly 210 215 220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr 225 230 235 240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala 245 250 255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr 260 265 270

His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln 275 280 285

Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val

290

300

295

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Asn P	Pro	Gln	Pro	Gly 170	Ile	Ala	Ala	Ala	Val 175	Glu	Leu	Leu	Ala	His 180	Asn	
aac g Asn A																691
ggt a Gly A	-		_			-			-	_	-	_				739
att g Ile G																787
ttt g Phe G 230	-		_	_		_		_			_					835
gcc g Ala G	-	-		_	_	-			-		-	-	_		_	883
gct g Ala G		_	-				_	-	_					-		931
cat c His P	_			_	_				_	_				-		979
aat g Asn V 2	-	_			_		_	_						-		1027
att g Ile A 310			_	_		_	_									1075
ctt a Leu I			_	_									-	_	_	1123
gga c Gly L					taad	ctcaa	acc (	ggtad	ccga	ca ti	Eg .					1161
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Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp

BGI-126CP - 567 -

35 40 45

Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
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Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe 65 70 75 80

Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu 85 90 95

Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly 100 105 110

Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val 115 120 125

Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly 130 135 140

Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile 145 150 155 160

Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu 165 170 175

Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro 180 185 190

Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala 195 200 205

Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr 210 215 220

Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly 225 230 235 240

Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
245 250 255

Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val 260 265 270

Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu 275 280 285

Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser 290 295 300

Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr 305 310 315 320

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ttaaaaaaaa accgtcgatt tcatttcctt ctcctattac atg tcc gta tgt gaa
                                                                   115
                                             Met Ser Val Cys Glu
gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc
                                                                   163
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly
                 10
gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt
                                                                   211
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val
             25
gat ecc etc ggt ttg egc atc gte etg aac aac tae tgg gag ege tgg
                                                                   259
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp
         40
                             45
cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg
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Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val
     55
ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc
                                                                   355
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile
70
aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag
                                                                   403
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys
                 90
                                      95
aag too tit gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc
                                                                   451
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser
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ctg gaa tcc taagaaataa aggtaggtgt cac
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Leu Glu Ser
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Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu
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25

20

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Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn 35 40 45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu

55

Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn
65 70 75 80

Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu 85 90 95

Lys Arg Tyr Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala 100 105 110

Thr Asn Gly Glu Ser Leu Glu Ser 115 120

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cctggaaatt ttcccacact aagtcaggtc taagtagggt atg gat atg acg att 115

Met Asp Met Thr Ile

1 5

tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca  $\phantom{0}$  163 Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro  $\phantom{0}$  10  $\phantom{0}$  15  $\phantom{0}$  20

gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211 Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu 25 30 35

ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr
40 45 50

gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307 Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe

ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu
70 75 80 85

gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403 Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala 90 95 100

gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451

VUI	Val	Lys	Glu 105	Gly	Asp	Ala	Asn	Arg 110	Leu	Leu	Gln	Glu	Ile 115	Val	Ala	
														ctc Leu		499
														gcg Ala		547
														cac His		595
			-		_		_	_			_	_	_	gct Ala 180		643
														tgg Trp		691
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gac																795
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Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr 130 135 140

Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser 145 150 155 160

Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val
165 170 . 175

Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly 180 185 190

Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr 195 200 205

Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu 210 215 220

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<212> DNA

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<223> RXA00195

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ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt  $\phantom{0}$  163 Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val  $\phantom{0}$  10  $\phantom{0}$  15  $\phantom{0}$  20

att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211 Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly 25 30 35

ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259 Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu 40 45 50

gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307 Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile 55 60 65

tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355 Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys 70 75 80 85

att Ile	ctg Leu	gtg Val	gaa Glu	acc Thr 90	aca Thr	aag Lys	gcc Ala	gac Asp	act Thr 95	gtg Val	ctt Leu	aat Asn	gct Ala	ctg Leu 100	gtt Val	403
		_				gca Ala	_	_	-		-	_				451
						aaa Lys										499
-			_	_	_	ctg Leu 140		_			-	_	_	_		547
		_	_		_	tgt Cys	_	_	_			_	_		_	595
						gct Ala										643
	aga Arg	_	_			tgad	eteco	ega o	gcago	gcago	ca go	eg				684
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	)> 4(		T	Tle	T 0	T1 -	T = 1-	C1.:	0	m\r	C1	0	T1.	G1-	ml	

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr 1 5 10 15

Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val 20 25 30

Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala 35 40 45

Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln
50 55 60

Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly 65 70 75 80

Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val 85 90 95

Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr 100 105 110

Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val 115 120 125

Ala Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile

130 135 140 Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly 155 Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro 165 170 175 Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg 180 <210> 401 <211> 738 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(715) <223> RXA00196 <400> 401 ctgccatggc gcagtgtttg cgttcgggta ctcgtgatga ggttgcgcgg attgtgctga 60 cagcttcggg cggacctttc agggctggac cagggagaag atg tgg gag gtg act 115 Met Trp Glu Val Thr ccc gag cag gca gcg cac cca acg tgg gcg atg ggg cag atg aac 163 Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn 10 acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag 211 Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg 259 Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val 45 cat deg dag teg ate ate dae ted atg ate aeg tit aeg gat get geg 307 His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala 60 65 acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg 355 Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu 70 75 gcg ctt gat tgg cca cat cgg gtg ccg aag gct cag ccg gcg ctg gat 403 Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca 451 Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala 105 110 ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg 499 Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr 120 125

tac ccc gcg Tyr Pro Ala 135			Ala								
ttg cgc ggg Leu Arg Gly 150											
gtc ctc caa Val Leu Gln		Ser Gln									
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Leu Glu Leu 35	Ile Glu	Ala Thr	Leu 40	Leu	Phe	Glu	Thr	Asp 45	Ala	Asp	Leu
Ile Asp Val 50	Thr Val	His Pro 55		Ser	Ile	Ile	His 60	Ser	Met	Ile	Thr
Phe Thr Asp 65	Gly Ala	Thr Ile	Ala	Gln	Ala	Ser 75	Pro	Pro	Ser	Met	Lys 80
Leu Pro Ile	Ala Leu 85		Asp	Trp	Pro 90	His	Arg	Val	Pro	Lys 95	Ala
Gln Pro Ala	Leu Asp 100	Phe Thr	Ala	Ala 105	His	Thr	Trp	Ala	Phe 110	Glu	Pro
Val Asp Asp 115	Ala Ala	Phe Pro	Ala 120	Val	Gln	Leu	Ala	Arg 125	His	Val	Ala
Lys Gln Lys 130	Gly Thr	Tyr Pro 135		Val	Tyr	Asn	Ala 140	Ala	Asn	Glu	Glu
Ala Ala Glu 145	Ala Phe	Leu Arg 150	Gly	Arg	Ile	Lys 155	Phe	Pro	Gln	Ile	Val 160
Asp Val Val	Asp Glu 165		Gln	Gly	Ala 170	Ser	Gln	Phe	Ala	Gly 175	Val
Ala Ser His	Val Asp	Asp Ile	Leu	Ala	Thr	Glu	Ser	Glu	Ala	Arg	Ala

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ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta

Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa

Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys

140

547

595

150	155	160	165
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		gga cat aac caa aa Gly His Asn Gln Ly 255	
		tat gat ggc ccc at Tyr Asp Gly Pro Il 27	e Ile Val
		tac gcg cct gct ga y Tyr Ala Pro Ala Gl 290	
		c gtc atc gat ccg ct y Val Ile Asp Pro Le 305	• •
-		tgg acc tct gtg tt y Trp Thr Ser Val Ph 320	
		gaa aac gtt gtt gc Glu Asn Val Val Al 335	
		g tcc aag ttc gaa gc 1 Ser Lys Phe Glu Al ) 35	a Asn Phe
		get gag cag cac ge Ala Glu Gln His Al 370	
		a aaa cac cct gtg gt y Lys His Pro Val Va 385	
		gat cag ctg ctc at Asp Gln Leu Leu Me 400	

	_			_	cct Pro	_		_			_	_			_	1363
					gcg Ala					-		_	-		_	1411
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	-		_	_	gac Asp			_	-		-		_	-	_	1603
					acc Thr		_				-					1651
_			_	-	act Thr	-	-		_	-	_					1699
					gtc Val											1747
	_	_		_	gtc Val 555		_		_	_		-				1795
					gtc Val											1843
					tct Ser											1891
			_		ctg Leu	_				_		_			-	1939
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<211> 636

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<213> Corynebacterium glutamicum

<400> 404

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Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu 20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn 165 170 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala 180 185 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys 195 200 205

Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala 210 215 220

Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu 225 230 235 240

Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His 245 250 255

Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp 260 265 270

Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala 275 280 285 Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile
290 295 300

Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr 305 310 315 320

Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn 325 330 335

Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys 340 345 350

Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu 355 360 365

Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His  $370 \hspace{1.5cm} 375 \hspace{1.5cm} 380$ 

Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln 385 390 395

Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu
405 410 415

Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val 420 425 430

Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala 435 440 445

Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser 450 455 460

Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro 465 470 475 480

Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu 485 490 495

Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser 500 505 510

Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val 515 520 525

Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro 530 535 540

Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp 545 550 555 560

His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val 565 570 575

Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro 580 585 590

Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg
595 600 605

Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr

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gaa gad Glu Asp 210	Āla		-	_	_			_	-				_		672
atc att Ile Ile 225		_			_	_		_	_		_	_	_		720
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att gto Ile Val			_	_		_	-		_		-	_		_	816
ctc gtg Leu Val															864
ttg ctc Leu Leu 290	Ser					-							_	_	912
caa atc Gln Ile 305	_			_	_		_	_				_		-	960
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Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu 50 55 60

Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His 65 70 75 80

Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val 85 90 95

Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu 100 105 110

Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg 115 120 125

Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp 130 135 140

Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg 145 150 155 160

Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp 165 170 175

Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro 180 185 190

Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr 195 200 205

Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu 210 215 220

Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser 225 230 235 240

Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp 245 250 255

Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp 260 265 270

Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser 275 280 285

Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg 290 295 300

Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu 305 310 315 320

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BGI-126CP

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cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag

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691

703

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<213> Corynebacterium glutamicum

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Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
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Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
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Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val 130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn 145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Asn Asp Asn 165 170 175

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		_			tat Tyr 235	_					_				_	835
				-	gaa Glu	-		-				_				883
					atc Ile			-	-		-		_	_	_	931
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					tgt Cys											1219
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					gtg Val		_			-				_	_	1363
		-			cag Gln							-		_		1411
					tgg Trp											1459
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			_			cgt Arg			_			_				1699
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Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe 50 55 60

His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val 65 70 75 80

Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro 85 90 95

Ala Asp Val His İle Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser 100 105 110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp 115 120 125

Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His 130 135 140

Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile 145 150 155 160

Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro 165 170 175

Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser 180 185 190

Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val 195 200 205

Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala 210 215 220

Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg 225 230 235 240

Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe 245 250 255

Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala 260 265 270 Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp 280 Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro 295 Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu 305 310 315 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr 325 330 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu 340 345 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro 425 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly

475 Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr 505

470

Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly

Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg

Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His 555

Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu 565 570

Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala 580 585 590

Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg 615 Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu 645 Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp 705 <210> 411 <211> 2223 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2200) <223> FRXA00879 <400> 411 aaaagatgta ttttctaaca aacttaccct cacgctacaa atatgctgtg cccacacgct 60 attagtggca taatgttgtg ttgtgactgc tcgcagattt ttg aat gaa ctc gcc 115 Leu Asn Glu Leu Ala gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat 163 Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt 211 Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc 259 Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg 45 caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca 307 Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro 60 tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg 355 Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val 75 80

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						cac His						547
						ccg Pro						595
						ggt Gly						643
						atg Met						691
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						ctg Leu			 _			787
_				_		atc Ile	_			 _	_	835
						ctt Leu						883
						cgc Arg						931
						gct Ala 285						979
						agc Ser						1027
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	cgc Arg															1171
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Arg 65	Pro	Leu	Pro	Pro	Ser 70	Val	Val	Ala	Val	Glu 75	Gly	Asp	Glu	Leu	Val 80	
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Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser 435 Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val 455 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp 465 470 475 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg 535 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu

Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr 625 630 635 640

Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln 645 650 655

Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys 660 665 670

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aac gcc Asn Ala															979
ggt gag Gly Glu 295															1027
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gcg acc Ala Thr	Leu H														1171
gat cac Asp His	-		_					-				-		-	1219
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Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys 1 5 10 15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe 20 25 30 .

Leu Gl<br/>n Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala<br/>  $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$ 

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr 65 70 75 80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His  $85 \hspace{1cm} 90 \hspace{1cm} 95$ 

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala 100 105 110

Leu Ala Ala Gl<br/>n Val Glu As<br/>n Leu Ile Pro Leu Cys Glu Glu Gly Leu 115 120 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys 130 135 140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu 145 150 155 160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val 165 170 175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala 180 185 190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr  $195 \hspace{1.5cm} 200 \hspace{1.5cm} 205 \hspace{1.5cm}$ 

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr 210 215 220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro 225 230 235 240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr 245 250 255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp 260 265 270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala 275 280 285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr 290 295 300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly 305 310 315 320

Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly 325 330 335

Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys 340 345 350

Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn 355 360 365

Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile 385 <210> 415 <211> 1287 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1264) <223> FRXA00043 <400> 415 aacagcaggc ctcaagtccg aagataatta acctaaatcc gtagacataa gacatcatac 60 gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg 115 Met Ala Glu Val Val 1 cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga 163 His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg 10 att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac 211 Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn 25 259 ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly 45 tto cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat 307 Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His 55 aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag 355 Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln 75 gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg 403 Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg 451 Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val 110 gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac 499 Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His 125 ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg 547 Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro 140

gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat

595

Asp 150	Phe	Ile	Phe	Pro	Gly 155	Asn	Pro	Thr	Asp	Leu 160	Ala	Gln	Val	Ile	His 165	
gcg Ala	gga Gly	aaa Lys	ggt Gly	tgg Trp 170	atc Ile	aaa Lys	tcg Ser	atc Ile	aca Thr 175	gta Val	gcg Ala	ccg Pro	gaa Glu	act Thr 180	gac Asp	643
aat Asn	ctt Leu	act Thr	gag Glu 185	ctt Leu	ctc Leu	gat Asp	ctc Leu	tgc Cys 190	gca Ala	gcg Ala	cac His	cac His	atc Ile 195	att Ile	gct Ala	691
														gca Ala		739
gcc Ala	ttg Leu 215	gct Ala	aaa Lys	gaġ Glu	aaa Lys	aat Asn 220	gtg Val	acg Thr	gtc Val	acg Thr	gct Ala 225	acg Thr	cat His	ttg Leu	ttc Phe	787
aat Asn 230	gcg Ala	atg Met	cct Pro	ccg Pro	ctg Leu 235	cat His	cat His	agg Arg	gat Asp	ccc Pro 240	ggc Gly	agc Ser	gtg Val	ggc Gly	gct Ala 245	835
ttg Leu	ctt Leu	gct Ala	gcg Ala	gca Ala 250	cgt Arg	gcc Ala	GJÀ ààà	gac Asp	gca Ala 255	tat Tyr	gtt Val	gag Glu	ttg Leu	atc Ile 260	gcc Ala	883
gac Asp	ggc Gly	gtg Val	cat His 265	ttg Leu	gcc Ala	gat Asp	gga Gly	acg Thr 270	gtc Val	gat Asp	cta Leu	gct Ala	cgt Arg 275	tcc Ser	aac Asn	931
aac Asn	gcc Ala	ttt Phe 280	ttc Phe	atc Ile	acg Thr	gac Asp	gcc Ala 285	atg Met	gaa Glu	gcc Ala	gcc Ala	gga Gly 290	atg Met	cca Pro	gac Asp	979
ggt Gly	gag Glu 295	tac Tyr	att Ile	ttg Leu	ggc Gly	gtt Val 300	ttg Leu	aac Asn	gtc Val	acc Thr	gtc Val 305	acc Thr	gat Asp	ggc Gly	gtc Val	1027
gcc Ala 310	Arg	ctg Leu	Arg	Asp	ggc Gly 315	Gly	gcc Ala	atc Ile	Ala	ggg Gly 320	Gly	acc Thr	agc Ser	aca Thr	cta Leu 325	1075
gcg Ala	agt Ser	cag Gln	ttc Phe	gtg Val 330	cac His	cac His	gtg Val	cgc Arg	agg Arg 335	ggt Gly	atg Met	acg Thr	ctt Leu	atc Ile 340	gac Asp	1123
gcg Ala	acc Thr	ctc Leu	cac His 345	acc Thr	tca Ser	acc Thr	gtc Val	gcc Ala 350	gcc Ala	aaa Lys	att Ile	ctc Leu	gga Gly 355	ctt Leu	agc Ser	1171
gat Asp	cac His	gaa Glu 360	atc Ile	gtt Val	aaa Lys	tcc Ser	aac Asn 365	cct Pro	gta Val	aat Asn	ttt Phe	gtg Val 370	gtc Val	ttt Phe	gac Asp	1219
tca Ser	aac Asn 375	ggc Gly	cag Gln	tta Leu	caa Gln	cag Gln 380	gtc Val	cat His	tta Leu	gac Asp	cat His 385	caa Gln	gta Val	att Ile		1264
taaa	tacg	ag c	aaaa	cttt	c ct	g										1287

<210> 416

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys 1 5 10 15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe 20 25 30

Leu Gl<br/>n Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala<br/> 35 40 45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr 65 70 75 80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
85 90 95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala 100 105 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
115 120 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys 130 135 140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu 145 150 155 160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val 165 170 175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala 180 185 190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr 195 200 205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr 210 215 220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro 225 230 235 240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr 245 250 255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp 260 265 270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala 275 280 285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr 295 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly 305 310 315. Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly 325 330 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys 340 345 Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn 360 Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile 385 <210> 417 <211> 1584 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1561) <223> RXN01752 <400> 417 gaaatgacgt gaccatcgat accaataccc aattgaaaga tcttgacctg gtcagccaag 60 ttggccgtca gatcgtggca gaacaacagg tggggaggtc atg atg gaa caa gat 115 Met Met Glu Gln Asp 1 ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163 Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys 10 15 aag get gea etg att gat gee att gaa ggg tta agg gtg ege gat eeg 211 Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro 25 cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc 259 Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe 45 att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa 307 Ile Ala Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln 55 60 gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att 355 Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile 70 75 80 aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403 Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu

90 95 100 tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac 451 Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp 105 110 aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag 499 Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu 120 gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys 135 140 cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg 595 His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp. Asp Leu Pro Thr 150 643 atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile 170 aag gtg ccg cca gcg cag ccc cgc acc aag ccg aag gcc tgt aac tat 691 Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr 185 190 gga ttg cac ttt gcc acg ggg gaa att gtc acg atc ttt gac gcg gaa 739 Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr Ile Phe Asp Ala Glu 200 gac atg cca gat ccc ctc caa ctg cgt cgc gtg gtg gtg gca ttt gaa 787 Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val Val Ala Phe Glu 215 220 cgc tcg gct tcc aat acg gtg tgc gtc cag tca agg ttg tcg tat cga 835 Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser Arg Leu Ser Tyr Arg 230 aac gcc agg cag aat ctg cta act gcg tgg ttc acc att gaa tat gac 883 Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp gtg tgg ttt aac ttc ctg ctg cca ggc gtc atg cgc atg aac gca cct 931 Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met Arg Met Asn Ala Pro 265 270 gtc cca ttg ggc ggt acc tcc aac cat ctg ctc acg ggt gtc ctg aaa 979 Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys gat ctc ggc gcg tgg gat cct ttc aat gtc aca gaa aat gcc gac ctc 1027 Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu ggc gta ccc atc gcg gca aaa gga tat tcc acc gcg gtg ttg gat tcg 1075 Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser 315 320 gtg acg tgg gag gaa gca aac tcc gac acc atc aac tgg ttg cgc cag 1123 Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln 330 335

						ggc Gly							1171
_			_			gtc Val		-				_	 1219
_					_	gca Ala 380			-				1267
						tcg Ser							1315
						cca Pro							1363
-	_			_		gct Ala				_			 1411
_		_		_	-	ccc Pro	-	_			_	_	1459
						atg Met 460							1507
						tcc Ser							1555
	gcg Ala	taaq	gcggt	gc d	ccato	cgtca	aa a	cc					1584

<210> 418

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala 1 5 10 15

Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu 20 25 30

Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
35 40 45

Gln Lys Val Ala Phe Ile Ala Val Val Gly Phe Ile Leu Met Leu 50 55 60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr

65 70 75 80 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu 100 105 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala 120 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala 130 135 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr Ile Ala Ala Glu Ala Ala Gly Val Asp Gln 165 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val 215 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser 230 225 235 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met 265 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly 360 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile 370 375 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile 395 390

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Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr 405 Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe 425 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Ile 435 440 Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys 475 Thr Ala His Gly Leu Glu Ala 485 <210> 419 <211> 689 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (19)..(666) <223> FRXA01839 <400> 419 tteetgetge caggtgteatg ege atg aac gea eet gte eea ttg gge ggt 51 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp 15 20 gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala 30 gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr 60 65 aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp 85 80 90 tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu 95 100 105 atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr

	110					115					120				
ttg tcg Leu Ser 125	Leu														435
ttc cca Phe Pro 140								_		_	-			_	483
aat gct Asn Ala														_	531
gac ccc Asp Pro															579
ctc atg Leu Met	_		_		_			_			_		-	_	627
cca tcc Pro Ser 205	Tyr					-			-			taa	gcggt	:gc	676
ccatcgt	caa a	acc													689
<210> 4	20														
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<211> 2 <212> P <213> C <400> 4 Met Arg 1 Leu Thr	RT oryne 20 Met Gly Asp 35 Val	Asn Val 20 Ala	Ala 5 Leu Asp	Pro Lys Leu	Val Asp Gly	Pro Leu Val 40	Leu Gly 25 Arg	10 Ala Ile	Trp	Asp Ala	Pro Lys 45	Phe 30 Gly	15 Asn Tyr	Val Ser	
<211> 2 <212> P <213> C <400> 4 Met Arg	RT oryne 20 Met Gly Asp 35 Val	Asn Val 20 Ala Leu	Ala 5 Leu Asp	Pro Lys Leu Ser	Val Asp Gly Val 55	Pro Leu Val 40 Thr	Leu Gly 25 Arg	10 Ala Ile Glu	Trp Ala Glu	Asp Ala Ala 60	Pro Lys 45 Asn	Phe 30 Gly Ser	15 Asn Tyr Asp	Val Ser Thr	
<pre>&lt;211&gt; 2 &lt;212&gt; P &lt;213&gt; C &lt;400&gt; 4 Met Arg</pre>	RT oryne 20 Met Gly Asp 35 Val Trp	Asn Val 20 Ala Leu Leu	Ala 5 Leu Asp Asp	Pro Lys Leu Ser Gln 70	Val Asp Gly Val 55 Arg	Pro Leu Val 40 Thr	Leu Gly 25 Arg Trp	10 Ala Ile Glu Trp	Trp Ala Glu Tyr 75	Asp Ala Ala 60 Lys	Pro Lys 45 Asn	Phe 30 Gly Ser	15 Asn Tyr Asp Leu	Val Ser Thr Gln 80	
<211> 2 <212> P <213> C <400> 4 Met Arg	RT oryne 20 Met Gly Asp 35 Val Trp Leu	Asn Val 20 Ala Leu Leu Val	Ala 5 Leu Asp Asp	Pro Lys Leu Ser Gln 70 Met	Val Asp Gly Val 55 Arg	Pro Leu Val 40 Thr Ser	Leu Gly 25 Arg Trp Arg	10 Ala Ile Glu Trp Lys 90	Trp Ala Glu Tyr 75 Trp	Asp Ala Ala 60 Lys Leu	Pro Lys 45 Asn Gly Val	Phe 30 Gly Ser Tyr	15 Asn Tyr Asp Leu Glu 95	Val Ser Thr Gln 80 Leu	
<pre>&lt;211&gt; 2 &lt;212&gt; P &lt;213&gt; C &lt;400&gt; 4 Met Arg</pre>	RT oryne 20 Met Gly Asp 35 Val Trp Leu Ile	Asn Val 20 Ala Leu Val Pro 100	Ala 5 Leu Asp Asp Tyr 85 Ala	Pro Lys Leu Ser Gln 70 Met	Val Asp Gly Val 55 Arg Arg	Pro Leu Val 40 Thr Ser Arg	Leu Gly 25 Arg Trp Arg Pro	10 Ala Ile Glu Trp Lys 90 Phe	Trp Ala Glu Tyr 75 Trp Leu	Asp Ala Ala 60 Lys Leu Met	Pro Lys 45 Asn Gly Val	Phe 30 Gly Ser Tyr Gln Gly 110	15 Asn Tyr Asp Leu Glu 95 Thr	Val Ser Thr Gln 80 Leu Pro	

Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile 150 145 155 Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu 165 Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala 180 185 Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu 200 Lys Thr Ala His Gly Leu Glu Ala <210> 421 <211> 1050 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1027) <223> RXA01859 <400> 421 tacgcccagg gtttccatat tggtaaatct aagccgattg atgaatttat agctacttat 60 ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc 115 Met Lys Lys Ser ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg 163 Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly 10 atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca 211 Met Gly Ile Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala 25 tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc 259 Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu 40 ttt qat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc 307 Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta 355 Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg 403 Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala 90 95 ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att 451 Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile 105 110

							gca Ala 125									499
			_	_	_		tca Ser						_	_		547
_	-	_	_	_		_	act Thr	-	_			_		-	_	595
							gaa Glu									643
							ttg Leu									691
		_			_		gtt Val 205	-	-			-		_		739
			_	_	_		cgc Arg	_		_		_	_	_		787
_	_				_		tac Tyr									835
							tac Tyr				_	_	_			883
							gtt Val									931
							gta Val 285									979
							tat Tyr									1027
taat	gagt	tg a	accct	ggct	t to	ga										1050
<211 <212	)> 42 l> 30 2> PE 3> Co	) 9 RT	ebact	eriu	ım gl	Lutam	nicum	ı								
	)> 42 Lys		Lys	Ser 5	Phe	Pro	Ile	Ala	Arg 10	Val	Ile	Gly	Ile	Gly 15	Val	

Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp 35 40 45

Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu 50 55 60

Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr 65 70 75 80

Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu 85 90 95

Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val 100 105 110

Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu 115 120 125

Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu 130 135 140

Pro Pro Glu Arg Ile Val Val Ala Asp Asn Cys Thr Asp Glu Thr 145 150 155 160

Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn 165 170 175

Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met 180 185 190

Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp 195 200 205

Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Phe Glu 210 215 220

Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser 225 230 235 240

Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr 245 250 255

Ser Arg Asp Ile Tyr Arg Arg Gly Arg Val Phe Val Leu Thr Gly
260 265 270

Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser 275 280 285

Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala 290 295 300

Gly Val Asp Arg Arg 305

<210> 423

<211> 882

<212> DNA

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<213> Corynebacterium glutamicum

<220>

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	r Lys Gly Gly	acc ttg ggg ctt Thr Leu Gly Leu 30		
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		gtt caa atc ctt Val Gln Ile Leu 125		
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	r Arg Ala Gln	aac atc gtg ttg Asn Ile Val Leu 190		

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Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu 50 55 60
Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys 65 70 75 80
Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu 85 90 95
Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala 100 105 110
Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu 115 120 125
Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser 130 135 140
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Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala 165 170 175
Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu 180 185 190
Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu

195 200 205 Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn 215 Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn 225 230 235 Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg 245 <210> 425 <211> 1998 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1975) <223> RXA01482 <400> 425 ttgcgtgctg caacttaatt atggtcctcc cagctcagtg tgctgtgtgg attgtttatt 60 ctcgtccatt aagtgatcga gaaaaagttg ttgtaaagtc atg cgc atg tgt gga 115 Met Arg Met Cys Gly att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163 Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat 211 Leu Asp Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr gac too goa ggt att gct att cac gcc aat ggt gag att agc tac cga 259 Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg 45 307 aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act 355 Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr 70 75 cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat 403 His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn 95 ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa 451 Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu 105 110 115 ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc 499 Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr 120 125 130

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							aat Asn									787
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							atc Ile									1171
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	_			_			ctg Leu		_	_	_	_	_			1411
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tegetteteg acg 1998

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Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala
50 .55 .60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His
65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro \$85\$ 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile 100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn 115 120 125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu 130 135 140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu 145 150 155 160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala 165 170 175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val 180 185 190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly 195 200 205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val 210 215 220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser 225 230 235 240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala 245 250 255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln 260 265 270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly 275 280 Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser 295 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly 305 315 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu 325 330 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser 395 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala 425 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala 505 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn 570 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu

585

590

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gac cac ggt ctc cac gac acc gac acc cca ctg agc cac aaa gat Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp 165 170 175	
gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala 180 185 190	
gaa atg cat gcc ttc gaa gcc aac acc tac cgt tcg cgg aaa tgt Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys 195 200 205	
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Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr 100 105 110	
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Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala 130 135 140	
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala 145 150 155 160	
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp 165 170 175	

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Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys 

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gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct

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Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc tac cgt ttc gcg gaa atg 624 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg 210 215 220

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20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
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Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met 195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg 210 215 220

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_			_	_	_		tct Ser 40		_	-	_	-			_	144
							gat Asp									192
							gtg Val									240
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							gag Glu									336
							ttg Leu 120						-	-	-	384
-			-				aac Asn			_	_			_		432
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tgt																533

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Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
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Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
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Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
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Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
             20
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gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg

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					gga Gly 70											240
			_		aag Lys	-		_	_	-	_					288
					gca Ala											336
			_	-	cac His	_	_					_		_	_	384
					gtg Val											432
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tgt																533
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Ala	Ser	Asn 35	Leu	Ala	Ala	Asn	Ser 40	Lys	Met	Ala	Arg	Gln 45	Asn	Thr	Arg	
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Gly 65	Ala	Leu	Val	Leu	Gly 70	Pro	Val	Val	Gly	Thr 75	Leu	His	Ile	Lys	Phe 80	
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Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp 115 120 125

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln 130 135 140

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- gcg gaa cgt gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211 Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu 25 30 35
- tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259
  Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
  40 45 50
- aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307 Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
- gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355
  Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe
  70 75 80 85
- atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg
  Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
  90 95 100
- gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451 Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His 105 110 115

ccg gtc ga Pro Val As 12	p Asp													499
ccc att to Pro Ile Se 135														547
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gtg gtg ac Val Val Th	_	_		_	_	_			_					643
gcg cga gt Ala Arg Va														691
ctg cca ga Leu Pro Gl 20	u Gly													739
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ggcactaaga	aga													798
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Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val 155 Ile Gly Ala Gly Pro Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg 180 185 190 Leu Glu Arg Ser Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly 200 Ile Leu Pro Thr Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys 210 215 Tyr 225 <210> 437 <211> 891 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(868) <223> RXA02666 <400> 437 gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60 tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115 Met Ser Ser Thr Arg atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163 Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu 15 10 ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu 25 30 tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu 40 45 atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu 55 355 ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg 70 75 ctc gtg cac ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403

Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu

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		ca cca ccc ggc atg nr Pro Pro Gly Met 25	
		cc acc gca gtc atc La Thr Ala Val Ile 145	
		g tcc cct gat ggc al Ser Pro Asp Gly 160	
Asp Thr Pro Asn		et ege gee gte caa eu Arg Ala Val Gln 175	
, ,		ca gcg aat gag aaa a Ala Asn Glu Lys 190	3 3
		cc gat gac gcc agc nr Asp Asp Ala Ser 05	
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Glu Ser Val Asp	Glu Ile Ile Il	e Leu Val Ser Pro	Asp Met Glu Thr

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Val	Trp	Ala	Gly 100	Leu	Gln	Ala	Ile	Ser 105	Leu	Asp	Asp	Ala	Thr 110	Pro	Asp
Ala	Ile	Val 115	Leu	Ile	His	Asp	Ser 120	Ala	Arg	Ala	Leu	Thr 125	Pro	Pro	Gly
Met	Ile 130	Ala	Arg	Val	Val	Arg 135	Lys	Val	His	Glu	Gly 140	Ala	Thr	Ala	Val
Ile 145	Pro	Val	Leu	Pro	Val 150	Ser	Asp	Thr	Ile	Lys 155	Arg	Val	Ser	Pro	Asp 160
Gly	Gly	Val	Val	Val 165	Asp	Thr	Pro	Asn	Arg 170	Ala	Glu	Leu	Arg	Ala 175	Val
Gln	Thr	Pro	Gln 180	Gly	Phe	Leu	Leu	Ser 185	Glu	Leu	Val	Ala	Ala 190	Asn	Glu
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Pro 225	Met	Ala	Phe	Lys	Val 230	Thr	Thr	Pro	Ile	Asp 235	Met	Met	Leu	Ala	Glr 240
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ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163 Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala

10 15 20 tgc aac cgt qaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211 Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259 Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val 40 307 cag ctt cgt gat ggc cag gaa aag gct gat gaa ttg ggc gtg acc Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355 Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403 Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro act gat tot gat got gtg gtg ccg tcg gtg gaa got ctc aac cag got 451 Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala 110 gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg 499 Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct 547 Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg 595 Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu 155 caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt 643 Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe 170 gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag 691 Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln 190 acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg 739 Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu 205 ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag 787 Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu 220 atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat 835 Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt 883 Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val 250 255

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gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn 295 300 305	1027
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Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala 65 70 75 80	
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Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu 100 105 110	
Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser 115 120 125	
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Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp 165 170 175	
Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser 180 185 190	
Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp	

195 200 205 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe 215 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala 225 230 235 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr 295 Val Lys Leu Asp Asn Val Ala Asp Phe Lys 310 <210> 441 <211> 963 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(940) <223> RXA02440 <400> 441 gctgttaatc acgggttgtt cagctaccgg gggagcacca cgggcaacag atggggcatc 60 aggeggagga accgtegata egecteggtt ggttgtegeg atg gtg age eac gge 115 Met Val Ser His Gly gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163 Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211 Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu 25 atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259 Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val 40 45 gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307 Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val 55 60 gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355 Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala 70 75 80

	_		_			gat Asp			_							403
						gca Ala										451
						tgt Cys										499
_	_	-	_	_		ggc Gly 140			_		_				_	547
_		_		_		ggc Gly	_	_								595
						caa Gln										643
						atg Met										691
		_		_		gcc Ala			_			_	_		_	739
						aag Lys 220										787
						gcc Ala										835
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Ile Asp Ser Arg Val Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln 50 55 60

Ser Leu Gly Pro Val Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val 65 70 75 80

Val Gly Leu Asn Ala Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr 85 90 95

Gly Phe Phe Gly Gln Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala 100 105 110

Arg Leu Ala Glu Glu Asn Ala Gln Lys Val Leu Cys Val Ile His Glu
115 125

Gln Gly Asn Ser Ser Gln Glu Ala Årg Cys Gly Gly Val Ser Glu Gly 130 135 140

Leu Gly Lys Gln Val Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr 145 150 155 160

Ser Val Asn Ser Thr Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile 165 170 175

Asp Trp Val Val Gly Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp 180 185 190

Ala Ala Asp Ala Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr 195 200 205

Asn Ala Gln Leu Met Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala 210 215 220

Ile Asp Gln Gln Pro Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu 225 230 235 240

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- 635 -

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ttc ccc gtc cac Phe Pro Val His 25	Gly Asp Asn			
cgc acc aag atg Arg Thr Lys Met 40				
aac aac atg agt Asn Asn Met Ser 55	•	Thr Ala Gly Th		_
gct gag ccg tgg Ala Glu Pro Trp 70		· Val Ser Val Al		
gga gct tgg gtg Gly Ala Trp Val				
gta acg caa aaa Val Thr Gln Lys 105	Ile Thr Pro			
gtg gca aac ggc Val Ala Asn Gly 120				
ctc gtc aac gat Leu Val Asn Asp 135		Pro Asp Ala Hi		
ctc aac atg atc Leu Asn Met Ile 150		Leu Pro Ile Th		
gat aaa aaa cat Asp Lys Lys His				
aag gtt ctc gtg Lys Val Leu Val 185	Val Gly Ala			
gcg cag ttc cca Ala Gln Phe Pro 200				

		gat Asp													787
		gcc Ala													835
		gcg Ala													883
		cgc Arg													931
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		ggc Gly													1027
		gca Ala													1075
_		aat Asn			_	_					_	_	_		1123
		cca Pro					-			-					1171
	-	atc Ile 360	-	-					_				_	-	1219
		acc Thr							_		_	_		_	1267
		gcc Ala													1315
		gcc Ala													1363
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Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr 145 150 155 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr 165 170 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gln Leu 180 185 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg 195 200 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys 210 215 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln 225 230 235 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Val 245 250 255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His 260 265 270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu 275 280 285 Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala 295 Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr 315 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser 325 330 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly 345 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu 355 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu 440 Lys Glu Leu Ser Lys 450 <210> 445 <211> 449 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(426) <223> FRXA01569 <400> 445 gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc gat ggc 48 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp 40 atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly 55

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gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser 100 105 110	336
gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr 115 120 125	384
tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys 130 135 140	426
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ttc ccc gtc Phe Pro Val	,,,,,	, , , ,	Trp Phe			-
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gct gag ccg Ala Glu Pro 70						
gga gct tgg Gly Ala Trp				-		_
gta acg caa Val Thr Gln			. Gly Val			
gtg gca aac Val Ala Asn 120						
ctc gtc aac Leu Val Asn 135		_		-	_	
ctc aac atg Leu Asn Met 150					Ser Glu	
gat aaa aaa Asp Lys Lys		_	_	_	_	_
aag gtt ctc Lys Val Leu			Gln Leu			

gcg cag ttc Ala Gln Phe 200						Gln					739
acc tca gat Thr Ser Asp 215					Lys (						787
ata aac gcc Ile Asn Ala 230	-		-		_	_	_		_	_	835
gca gca gcg Ala Ala Ala			_			-		_	_		883
tcg cgc gcg Ser Arg Ala			Pro :		-	-					931
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Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His 135 Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr 155 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr 170 165 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu 180 185 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg 195 200 205 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys 215 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln 225 230 235 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr 260 265 Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro 295 Ala Thr Ser 305 <210> 449 <211> 1056 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1033) <223> RXA00825 <400> 449 cccgttcatg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60 tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt Met Arg Thr Val Val acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile 10 15 aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211 Lys Glu Gly His Glu Val Val Ile Asp Asn Leu Ser Arg Gly Arg

25 30 259 ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val 45 gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac 307 Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His 70 75 tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr atc ege atc get gac get gee ege eag eac ggt gtt ege aag gtt gte 451 Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val 105 499 ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro 120 gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc 547 Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser 135 aag gtg too ggt gaa att tac ctg aac acc tto cgc cac ctg tac ggc 595 Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly 150 155 tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa 643 Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln 170 gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt 691 Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu 185 ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc 739 Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Asn Thr Arg 200 205 gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct 787 Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser 220 ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa Gly Glu Ile Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 235 240 ace tet gae ege eag etg eac ace ete gtg gee act geg gea ggt tee 883 Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc 931 Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 1027 gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg 300 305 act cac taggggaaaa tccaccacaa atc 1056 Thr His 310 <210> 450 <211> 311 <212> PRT <213> Corynebacterium glutamicum <400> 450 Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser 135 Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val 165 Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile 185 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp 195 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala

215

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Glu Arg Phe Asn Ile 225 230 235 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala 245 250 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu 260 265 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr 295 Val Glu Tyr Phe Arg Thr His 305 310 <210> 451 <211> 1140 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1117) <223> RXA02054 <400> 451 cctaatqaac aqccqqaqca ccctqqtcqt ttqcaqaata qqcqcatcqa caacaqctac 60 taactctqcc agctcqcccq gacqaactaa qqtaqacqqc atq act tct ttq ctt Met Thr Ser Leu Leu gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr qta qaq caq cac cct qaa tac acc cac atc acg gtg ctg gat aaa ctc 211 Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu 25 acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa 259 Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys 40 45 gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc 307 Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser 55 60 ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac 355 Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His 70 75 80 aac gac aac too oto aac gac ooc too oog ttt gtt cac act aac oto Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu 90 95

							gaa Glu							451
							gaa Glu 125							499
							acc Thr							547
							tct Ser							595
							acc Thr							643
			_			_	aag Lys			-				691
							aaa Lys 205							739
							gat Asp							787
	_	_		_			gaa Glu				 _	_		835
-					_	_	gtc Val				 _		_	883
							gag Glu							931
							tcc Ser 285							979
							gtt Val							1027
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Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly 35 40 45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala 50 55 60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe 65 70 75 80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe 85 90 95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg 100 105 110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly 115 120 125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr 130 135 140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu 145 150 155 160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn 165 170 175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro 180 185 190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
195 200 205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp 210 215 220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile 225 230 235 240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu 245 250 255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala 260 265 270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu 275 280 285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly 290 295 300

Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu 305 310 315 320

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gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac  $\,$  163 Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr  $\,$  10  $\,$  15  $\,$  20

acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt 211 Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly 25 30 35

ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac  $\phantom{0}$  259 Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp  $\phantom{0}$  45  $\phantom{0}$  50

gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac 307 Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp 55 60 65

gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat 355
Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn
70 75 80 85

gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag 403 Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu 90 95 100

tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat 451
Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp
105 110 115

gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc 499 Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser

		120					125					130				
gct t Ala T 1																547
cgc g Arg G 150																595
ccg t Pro P																643
gat g Asp G		Phe														691
gat a Asp A		_		_						_		-			-	739
atg a Met S 2																787
ttt g Phe A 230																835
gag t Glu T		_	_	_			_		_	_						883
ccc t Pro	aga	itcaç	gtt t	tagt	tagtt	cc ct	c									909
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Gly P	Phe	Ala 35	Phe	Gly	Phe	Leu	Thr 40	Ala	Leu	Ala	Leu	Gly 45	Ala	Asn	Ala	
Val T	50	Cys	Thr	Asp	Asp	Asp 55	Gly	Arg	Pro	Glu	Gly 60	Pro	Gly	Val	Leu	
Lys T 65	hr	Leu	Ile	Asp	Ala 70	Ala	Ser	Arg	His	Asn 75	Leu	Glu	Glu	Val	Ser 80	

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu

				85					90					95		
Arg	Arg	Gly	Leu 100	Glu	Trp	Arg	Arg	Met 105	Arg	Ser	Glu	Leu	Ile 110	Asp	Pro	
Ala	Asn	Pro 115	Glu	Asp	Asp	Leu	Leu 120	Pro	Gly	Ile	Ala	Ser 125	Leu	Phe	Asn	
Gly	Ala 130		Ile	Ser	Ala	Tyr 135	Ala	Met	Glu	Arg	Ile 140	Gly	Val	Pro	Asp	
Tyr 145	Arg	Leu	Phe	Ile	Arg 150	Gly	Asp	Glu	Val	Glu 155	Tyr	His	Arg	Arg	Leu 160	
Val	Arg	Ser	Gly	Leu 165	Pro	Phe	Gly	Thr	Cys 170	Leu	Thr	Thr	Ala	Tyr 175	Leu	
His	Pro	Asp	Gly 180	Ser	Asp	Glu	Phe	Lys 185	Pro	Ile	Leu	Gly	Gly 190	Arg	Met	
His	Thr	Gln 195	Tyr	Pro	Asp	Asn	Asp 200	Phe	Lys	Arg	Phe	Phe 205	Thr	Tyr	Arg	
Asn	Arg 210	Gly	Tyr	Leu	Met	Ser 215	Gln	Pro	Gly	Met	Arg 220	Lys	Leu	Leu	Pro	
Gln 225	Glu	Tyr	Ala	Arg	Phe 230	Ala	Trp	Phe	Phe	Leu 235	Val	Gln	Lys	Arg	Asp 240	
Val	Lys	Gly	Phe	Arg 245	Glu	Trp	Leu	Arg	Leu 250	His	Lys	Leu	Gly	Arg 255	Asp	
Glu	Lys	Phe	Asn 260	Arg	Pro											
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gcg	cagto	gag t	tgat	tgat	to ca	agcca	aacco	c gga	aggat	gat	_	_	_	ggc Gly		115
	tcc Ser															163
	ggc Gly															211

tat cac cgc Tyr His Arg 40												259
acc acg gcg Thr Thr Ala 55												307
ctg ggt ggg Leu Gly Gly 70			-		_	-				_		355
ttt ttc acc Phe Phe Thr	_				_	-		-			-	403
cgc aag ctt Arg Lys Leu												451
gtt cag aaa Val Gln Lys 120												499
aaa ctg ggc Lys Leu Gly 135		Glu L					taga	atcaç	gtt t	tagt	agttc	552
ctc												555
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                                                                   115
                                             Met Ile Gln Ala Ala
                                               1
ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg
                                                                   163
Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu
                 10
gtt ttt gtc agc gcc atc atg ttc gcg att tcc ttt agc tcc ccc gtg
                                                                   211
Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val
             25
gcg aac ttc ggt ttc gat acg atc tgc gaa aaa ctc gac cgc gtc
                                                                   259
Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys Leu Asp Arg Arg Val
         40
                                                                   307
atg gtc gcc ggc acc ggc atg gcc aac atg agc gcc tac att tgc gcg
Met Val Ala Gly Thr Gly Met Ala Asn Met Ser Ala Tyr Ile Cys Ala
atg ctg gcc aca caa atc atc gga ttt tta ctc gac tgg aac gcc gac
                                                                   355
Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu Asp Trp Asn Ala Asp
ggc cac gcc tac acc tgg tcg aat ttc cag gtg gcg tgg ctt ggt ctg
                                                                   403
Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val Ala Trp Leu Gly Leu
                 90
ggc gcg gtg tgg ctg gca ggc atg atc ggg ctt gca gtc tgc ctc ctg
                                                                   451
Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu Ala Val Cys Leu Leu
            105
                                110
ctg cag cgt cga aaa aat att gct ttt cga cgc taaaacccga ccgtaaccgc 504
Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
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tag
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Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
35 40 45

Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser 50 55 60

Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu 65 70 75 80

Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$ 

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Ala Val Cys Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg 115 120 125

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<211> 615

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<223> RXA00328

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ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc  $\,$  163 Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys  $\,$  10  $\,$  15  $\,$  20

gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211 Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly 25 30 35

gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cgg ttg gcc gtg 259 Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val 40 45 50 BGI-126CP - 654 ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg 307 Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc 355 Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Ala Gly 80 get tta att ttg gea get gge eag ete att ttg ggt tte act gat tet 403 Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser 90 95 100 tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct 451 Tyr Met Ile Ala Ile Phe Ala Arq Val Leu Ile Ser Val Gly Asp Ser 105 110 tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg 499 Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met 120 125 tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg 547 Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val 135 140 ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct 592 Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro 150 155 615 tagggtggac aattcctttc gca <210> 460 <211> 164 <212> PRT <213> Corynebacterium glutamicum <400> 460 Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala

BGI-126CP

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Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr 145 150 155 160

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- agc cgc acc agc ttt ggt gtg gct gga gtg gag gcc att gat cgt ttt  $\,$  163 Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu Ala Ile Asp Arg Phe  $\,$  10  $\,$  15  $\,$  20
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- gtg tac gcg ttt gct cag att ccg atg ggc att ttg atc gat aag ttt 259 Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile Leu Ile Asp Lys Phe 40 45 50
- ggt cct cgg aag ctc ctt gcc att ggt gct ttg gtg atg ggt atc ggc 307 Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu Val Met Gly Ile Gly 55 60 65
- cag ctc att ttg ggc ttt acg gat agc tat tcc atc gcg att att gcc  $\,$  355 Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser Ile Ala Ile Ile Ala  $\,$ 70  $\,$ 80  $\,$ 85
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  Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His Thr Pro Ile Phe Thr
  105 110 115
- cag tta act acc tgc ctt ggc cag ttg ggc cag ttc ttt tct gcg gtg 499 Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln Phe Phe Ser Ala Val 120 125 130
- cct ttc atg gcg ttg ttg ggt gcg cag ggt tgg cct gtg gcg ttt gtc 547 Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp Pro Val Ala Phe Val

135 140 145 age ett ggt tee gtg gtg gea ete att geg ate gea geg etg gtg gee 595 Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile Ala Ala Leu Val Ala 150 155 gtt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag 643 Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln 170 175 gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc 691 Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg 185 190 aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg 739 Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val 200 787 tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu 215 ggc atg gga ctg tct gca acg gct ggt ttg gtg ttg agc atc aac 835 Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn 230 acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca 883 Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala 250 cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt 931 Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val 265 caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt 979 Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly 280 285 ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg 1027 Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala 295 300 gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag 1075 Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys 315 att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca 1123 Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser 330 tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg 1171 Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala 350 cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg 1219 His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala 365 att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga 1267 Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg 375 380

ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc 1315 Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr 390 395 400 405

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<211> 408

<212> PRT

<213> Corynebacterium glutamicum

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Ser Val Gl<br/>n Val Gly Val Tyr Ala Phe Ala Gl<br/>n Ile Pro Met Gly Ile 35  $\phantom{000}40\phantom{000}45$ 

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu 50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser 65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile 85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His 100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln 115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp 130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile 145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro 165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu 180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His 195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val 210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu 225 230 235 240

Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile 265 Ala Leu Ser Phe Val Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly Leu Met Ala Ile Ile Leu Val Asn Ile Val Met 290 295 300 Gly Leu Thr Thr Ala Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu 315 Arg Leu Asp Arg Lys Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly 375 Phe Val Val Ala Arg Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala 385 390 Gln Ile Arg Ser Thr Lys Asp Phe 405 <210> 463 <211> 2265 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2242) <223> RXN01554 <400> 463 tggcttaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaaa 60 tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg 115 Leu Lys Lys His Val acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163 Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu 10 15 ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211 Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro 25 30 gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc 259 Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser

40 45 50 gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc 307 Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly 55 age gae aaa gtt ete tat ace gaa gat get tta agt ate gaa gat gge 355 Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg 403 Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala 90 atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa 451 Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln gtt gaa cet tgt get eea ggt eag ttt gaa aag tte ace agt geg ege 499 Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg 120 atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act 547 Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr 135 gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg 595 Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp 150 155 atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc 643 Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu 170 tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg 691 Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser 185 cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc 739 Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val 200 205 aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc 787 Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu 215 gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val gag tac ttc att gat gag gcg att aac cgc cag tca tgg cgc aac 883 Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn 255 gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg 931 Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala 270 cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat 979 Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn 280 285 290

		agc gcc Ser Ala										1027
		cgg tcc Arg Ser 315										1075
		tct gaa Ser Glu 330										1123
	_	act ctg Thr Leu	_		-	_	_			_	_	1171
		gca agt Ala Ser	Ala A									1219
		aat ttg Asn Leu										1267
		gct gtc Ala Val 395										1315
_	-	tgt ctg Cys Leu 410	-									1363
_		gaa ccg Glu Pro		_					_		_	1411
		cac ctt His Leu	Pro G	-		-						1459
		cgg gcg Arg Ala										1507
_		atg cag Met Gln 475					_	-	_		_	1555
		ggt gaa Gly Glu 490							_		_	1603
		tac tcg Tyr Ser										1651
		ctt cgc Leu Arg	Gln M									1699

gat tgg cat ga Asp Trp His As 535						1747
acc att gac go Thr Ile Asp Gl 550						1795
aac tct gtt ac Asn Ser Val Th			-			1843
ttg tcg gaa ga Leu Ser Glu Gl 58	u Glu Tyr	Arg Glu V			p His Leu	1891
att ttg aac ac Ile Leu Asn Th 600					•	1939
gcg gtc gac aa Ala Val Asp As 615						1987
cat gtg gca gt His Val Ala Va 630						2035
gac gct gcg aa Asp Ala Ala As						2083
gat ggc agc ga Asp Gly Ser As 66	sp Leu Glu	Val Gly S			r Ala Glu	2131
acc gtg agc to Thr Val Ser Tr 680						2179
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Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val 35 Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg 50

Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu 65 70 75 80

Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val 85 90 95

Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn 100 105 110

Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys 115 120 125

Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe 130 135 140

Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val 145 150 155 160

Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala 165 170 175

Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser 180 185 190

Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys 195 200 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys 210 215 220

Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr 225 230 235 240

Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg  $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255$ 

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Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp 275 280 285

Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro 290 295 300

Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg 305 310 315 320

Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro 325 330 335

Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg
340 345 350

Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp

360 355 Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln 375 Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly 385 390 395 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp 410 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu 420 425 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg 570 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly 585 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His 615 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val 625 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly 650 645 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly 660 665 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu 680 685 675

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                                             Leu Gly Val Gly Thr
                                                                    163
cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag
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Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe
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                                  30
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ggc aag tot acg gtt ccg gtt ggt act gct gag cag ttg cag gag ott
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu
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gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat
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Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn
                                                                    355
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Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro
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gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att  $\phantom{0}$  259 Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile  $\phantom{0}$  40  $\phantom{0}$  45  $\phantom{0}$  50

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Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu
70 75 80 85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403 His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys 90 95 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451 Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp 105 110 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499 Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp

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Tyr Asn Gly P	_	Ile Glu Pr		gac ttc gat ga Asp Phe Asp Gl 195	
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<pre>&lt;212&gt; PRT &lt;213&gt; Coryneb &lt;400&gt; 468 Leu Asp Ala A</pre>	la Gly Ile 5 le Thr Asp 20 lu Val Ala he Ile Ala er Arg Thr 70 eu Leu His 85 al Lys Asp	Ser Leu Ser Pro Phe Gl 2 Lys Leu Ph 40 Glu Gly As 55 His Ala Me Glu Asn Gl Leu Ile Th	lu Asp His Leu 25 he Gly Ala Lys sp Asn Pro Glu 60 et Val Glu Leu 75 lu Lys Gly Ile 90 hr Ser Ile Asp	Ser Pro Asn Ty  Ser Pro Asn Ty  Ser Pro Asn Ty  Tyr Gly Asn Se	g t s y o r

Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile 145 150 155 Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu 180 185 Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr 200 Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu 215 Tyr Asn 225 <210> 469 <211> 687 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(664) <223> RXN03030 <400> 469 gaagatgaag cagaaaagat cattggtgcg ccagaggttt ctgcattggg caacaaagca 60 cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat 115 Val Leu Pro Leu Asp cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163 Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys 10 atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc 211 Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ile Arg Ala Glu Leu 25 cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc 259 Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile 40 45 gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt 307 Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly 55 gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc 355 Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403 Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe 95

20.	. 200.							·								
							gag Glu									451
							cca Pro 125									499
						_	ggc Gly	_	_		_		_		-	547
	_	_			_	-	tcc Ser							_		595
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	)> 47 Leu		Leu	Asp 5	Pro	Ala	Ala	Ser	Leu 10	Lys	Ile	Tyr	Pro	Leu 15	Val	
Thr	Gly	Arg	Thr 20	Lys	Ile	Asp	Glu	Val 25	Gln	Leu	Gln	Leu	Glu 30	Ala	Ala	
Ile	Arg	Ala 35	Glu	Leu	Pro	Gly	Val 40	Thr	Leu	Val	Ser	Ser 45	Glu	Ser	Glu	
Ala	Asp 50	Leu	Ala	Ile	Val	Trp 55	Ala	Arg	Pro	Glu	Ile 60	Ala	Leu	Phe	Glu	
Asp 65	Asp	Leu	Glu	Gly	Val 70	Ser	Leu	Ser	Val	Asp 75	Pro	Arg	Ala	Asn	Gly 80	
Val	Asp	Val	Glu	Arg 85	Val	Gln	Ala	Val	Glu 90	Ala	Ala	Val	Pro	Thr 95	Ile	

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu 120

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro 135

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp 145 150 155 160 Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala 165 170 175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe 180 185

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		-		-	-		ctc Leu	_	-		_				_	163
_		_			-	_	ctc Leu	_	-	-	_	-	_		-	211

gag cac att gaa tgg cag tcc agc tac cca gtc gcc ggc ctc ttc gca 259 Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val Ala Gly Leu Phe Ala

gct ggc ggt act ggc gaa gga ttc agc ctt acc gtt gag gaa aac cac 307 Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr Val Glu Glu Asn His 55 60 65

cgt gtc act caa ctt gca gtt cag gcg tcc agc ccg gaa gtt ccc gtg 355 Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser Pro Glu Val Pro Val 70 75 80 85

ttg ggg tct gct act ggc tca act aag tct gcc atc gca aac gca cag
Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala Ile Ala Asn Ala Gln
90 95 100

ggc gca gag gca gca ggc gct gaa ggt gtc ctc ctg ctt cct ccc tac 451 Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu Leu Pro Pro Tyr 105 110 115

ctc acc gaa tgc gac gca gaa ggc ctg tac aac cat gca gcc gca gtc 499 Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn His Ala Ala Ala Val 120 125 130

tgt gaa too act tot ott ggt gto ato gtg tao aac ogt goo aat goo 547 Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr Asn Arg Ala Asn Ala 135 140 145

ate tac tee cea gag gtt ate get ega ete tet gag ege tac eee aac 595

Ile Tyr Ser 150		al Ile Ala 55	-	er Glu Arg 60	Tyr Pro	Asn 165
ttc att gga Phe Ile Gly	_				_	-
atc acc acg Ile Thr Thr			-			
acc gct gag Thr Ala Glu 200	_		-	, , , ,		
tac tcc tct Tyr Ser Ser 215	-		-	-		
tac gcc gat Tyr Ala Asp 230	Val Arg A		Ser Ala Al			-
agc gat ttt Ser Asp Phe		_	-		-	
tac ggt gtc Tyr Gly Val	_					
gct ggc ggc Ala Gly Gly 280		_	-		-	
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Leu Leu Ser	Phe Pro A	la Thr Ala	Phe Gln As	sp Asp Leu	Glu Val 30	Asp
Glu Ala Ala 35	Tyr Val G	lu His Ile 40	Glu Trp Gl	ln Ser Ser 45	Tyr Pro	Val
Ala Gly Leu 50	Phe Ala A	la Gly Gly 55	Thr Gly Gl	lu Gly Phe 60	Ser Leu	Thr

Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser 65 70 75 80

Pro Glu Val Pro Val Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala 85 90 95

Ile Ala Asn Ala Gln Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu 100 105 110

Leu Leu Pro Pro Tyr Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn 115 120 125

His Ala Ala Ala Val Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr 130 135 140

Asn Arg Ala Asn Ala Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser 145 150 155 160

Glu Arg Tyr Pro Asn Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile 165 170 175

Glu His Leu Ala Lys Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr 180 185 190

Leu Gly Gly Leu Pro Thr Ala Glu Thr Phe Ala Leu Pro Leu Gln
195 200 205

Met Gly Met Ser Thr Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp 210 215 220

Phe Ala Leu Ser Phe Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala 225 230 235 240

Val Lys Gln Lys Leu Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg 245 250 255

Asp Arg Ala Gln Gly Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys 260 265 270

Ala Val Gly Arg Asn Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu 275 280 285

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Ala Gly Ser Tyr Arg Leu Gln Leu Arg 305 310

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<213> Corynebacterium glutamicum

<220>

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<223> RXN02125

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_			_		-		-				_	_	atg Met	 835
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	 tat Tyr			-	taga	aaaga	att (	tttat	cat	gg ga	ac			924

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Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
35 40 45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile 50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys 65 70 75 80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro 85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala 100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser 130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn 145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val 165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln · 180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys 195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala 210 215 220

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atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat

547

Ile	Asp 135	Gly	Asn	Leu	Asp	Val 140	Ile	Val	Arg	Gly	Glu 145	Val	Leu	Leu	Asp	
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													ctg Leu	-		739
				_	-						_		act Thr			787
	_			_		_	-						gcg Ala			835
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	_		_		_		-				_	_	aag Lys 275			931
_		-	_	_			-						ctt Leu		-	979
										Met			gtg Val			1027
													gtc Val			1075
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								_			_	_	ctc Leu 355	_		1171
													cgg Arg			1219
													gcc Ala			1267

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						 cgc Arg					 			2035
	_	_		_	-	gca Ala								2083
						tgg Trp	-					-		2131
						ctc Leu 685								2179
						gtc Val		_					_	2227
						gaa Glu								2275
_		_	_			acc Thr				-			_	2323
			-		_	 ctg Leu			_	_	_			2371
						gcg Ala 765								2419
						tgt Cys								2467
						ttc Phe								2515
						gat Asp								2563
						gac Asp								2611
						tcc Ser 845								2659
						aac Asn								2707

						_	cgc Arg	_				_	_			2755
				_			tgg Trp		_						_	2803
				_			gaa Glu			_	_		_	-	-	2851
				_		_	gca Ala 925		-		-			-		2899
							caa Gln									2947
							gaa Glu									2995
_							tgg Trp	_			_				_	3043
							gtc Val					-		_	_	3091
		_	Ğlu	-			gta Val 100	Āla	_	_		Pro	_	_		3139
		Āsp		_			gtc Val 20				Glu			-		3187
	Asp					Leu	caa Gln			Cys					Asp	3235 1045
					Thr		att Ile			Tyr				Pro		3283
				Ser			tcc Ser		Phe				Ala			3331
			Ğİy				gca Ala 108	Val				Tyr				3379
		Leu					ggc Gly O				Gly					3427
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Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp 1110 1115 1120 1125

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<400> 476

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Gly Leu Leu Gly Leu Leu Met Phe Val Leu Pro Phe Leu Pro Val
50 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala 85 90 95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu 100 105 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly 115 120 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly 130 135 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp 145 150 155 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu
165 170 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro 180 185 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala 195 200 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser 210 215 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile

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Ile	Leu	Asp	Gly 260	Arg	Lys	Ala	His	Arg 265	Phe	Leu	Pro	Ala	Asn 270	Trp	Tyr
Lys	Leu	Lys 275	Pro	Leu	Asp	Gly	Val 280	Val	Val	Ala	Ile	Leu 285	Val	Phe	Trp
His	Phe 290	Leu	Gly	Ala	Asn	Thr 295	Ser	Asp	Asp	Gly	Phe 300	Ile	Met	Thr	Met
Ala 305	Arg	Val	Ser	Gln	Asn 310	Ala	Asp	Tyr	Met	Ala 315	Asn	Tyr	Tyr	Arg	Trp 320
Phe	Gly	Val	Pro	Glu 325	Ser	Pro	Phe	Gly	Ala 330	Pro	Tyr	Tyr	Asp	Leu 335	Leu
Ala	Leu	Met	Ala 340	Tyr	Ile	Ser	Thr	Ser 345	Ser	Ile	Trp	Leu	Arg 350	Leu	Pro
Ala	Leu	Leu 355	Ala	Gly	Leu	Ile	Met 360	Trp	Phe	Val	Ile	Thr 365	Arg	Glu	Val
Met	Pro 370	Arg	Phe	Gly	Ser	Leu 375	Val	Asn	Gly	Arg	Arg 380	Val	Ala	His	Trp
Ser 385	Ala	Ala	Met	Val	Phe 390	Leu	Ala	Phe	Trp	Leu 395	Pro	Tyr	Asn	Asn	Gly 400
Thr	Arg	Pro	Glu	Pro 405	Ile	Ile	Ala	Met	Gly 410	Ala	Leu	Leu	Ala	Trp 415	Val
Ser	Phe	Glu	Arg 420	Ala	Ile	Ala	Thr	Ser 425	Arg	Leu	Leu	Pro	Ala 430	Ala	Ile
Gly	Val	Ile 435	Ile	Ala	Thr	Ile	Ser 440	Leu	Ala	Ser	Gly	Pro 445	Thr	Gly	Leu
Met	Ala 450	Val	Ala	Ala	Leu	Leu 455	Val	Ser	Leu	Ser	Ala 460	Leu	Ile	Arg	Ile
Leu 465	Tyr	Arg	Arg	Leu	Pro 470	Leu	Ile	Gly	Ala	Ser 475	Arg	Gly	Ala	Ser	Lys 480
Ser	Lys	Val	Phe	Gly 485	Ala	Ser	Met	Ala	Met 490	Leu	Ala	Pro	Phe	Leu 495	Ala
Ser	Gly	Thr	Ala 500	Ile	Leu	Ile	Ala	Val 505	Phe	Gly	Asp	Gln	Thr 510	Leu	Ser
Thr	Val	Met 515	Glu	Ser	Ile	Ser	Val 520	Arg	Ser	Ala	Lys	Gly 525	Pro	Ala	Leu
Thr	Trp 530	Tyr	His	Glu	Tyr	Val 535	Arg	Tyr	Gln	Thr	Val 540	Met	Glu	Gln	Thr
Val 545	Asp	Gly	Ser	Phe	Thr 550	Arg	Arg	Phe	Ala	Val 555	Leu	Met	Leu	Met	Ala 560

Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro 575

Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly 580

Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe 595 600 605

Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val 610 615 620

Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser 625 630 635 640

Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn 645 650 655

Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr
660 665 670

Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala 675 680 685

Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val 690 695 700

Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala 705 710 715 720

Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala 725 730 735

Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys
740 745 750

Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val 755 760 765

Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala 770 775 780

Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro 785 790 795 800

Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly 805 810 815

Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp

Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr 835 840 845

Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly 850 855 860

Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe 865 870 875 880

Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly 885 890 895

Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu 900 905 910

Ala Thr Glu Glu Ala Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile 915 920 925

Glu His Tyr Asp Ile Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met 930 935 940

Leu Glu Tyr Gly Arg Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly 945 950 955 960

Glu Ala Met Met Tyr Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu 965 970 975

Arg Tyr Pro Leu Asp Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile 980 985 990

Val Ala Thr Asp Val Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr 995 1000 1005

Pro Pro Arg Val Pro Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser 1010 1015 1020

Glu Thr Pro Gly Leu Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys 1025 1030 1035 1040

Gln Arg Thr Phe Asp His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr 1045 1050 1055

Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln
1060 1065 1070

Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn 1075 1080 1085

Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp 1090 1095 1100

Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala 1105 1110 1115 1120

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Trp Asn Pro Gly His Met Lys Val Asp Glu 1140 1145

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<223> RXN01175

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Tyr	Glu 215	Ala	Leu	Ala	Arg	Glu 220	Ile	Asp	Ser	Gly	Leu 225	Arg	Phe	Met	Glu	
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			_	_	_	-	-		gag Glu 255	_		_	_	_		883
									ctt Leu							931
									ggc Gly							979
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Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
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Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe 65 70 75 80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu 85 90 95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val 100 105 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala 115 120 125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu 130 135 140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu 145 150 155 160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala 165 170 175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala 180 185 190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser 195 200 205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly 210 215 220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala 225 230 235 240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg 245 250 255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr 260 265 270

Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met 275 280 Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly 295 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala 305 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala 325 330 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln 340 345 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe 370 375 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln 435 Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn 450 455 <210> 479 <211> 984 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(961) <223> RXN01376 <400> 479 tecteategg ttategggag tggeggatae ttettgeaaa ettaaaceae tatgettteg 60 cttcgtgagt actttgaaat cccccatcgc tgtgatcaca gtg acc tat tca cca 115 Val Thr Tyr Ser Pro ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser 10 cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211

Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val

25 30 35 cct gag cag gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259 Pro Glu Gln Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg 307 Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser 55 60 ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc 355 Leu Arg Ala Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu 70 gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg 403 Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu 90 ctt gaa tgt gcg aaa cgt cac cct gaa gca gcg gtt ggc ccg ttg 451 Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc 499 Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro 120 act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa 547 Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys 135 140 595 tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr 150 gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg 643 Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Arg Trp 170 gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac 691 Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr 185 190 739 atg gaa gac gtt gac ctg gga gat cgg ctg gtt cgc gcc ggt ttc acc Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr 200 aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt 787 Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val 220 gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg 835 Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt 931 Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val

984

ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg Gly Val Ser Lys Met Arg Thr Lys Ala Ser gac <210> 480 <211> 287 <212> PRT <213> Corynebacterium glutamicum <400> 480 Val Thr Tyr Ser Pro Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser Leu Arg Ala Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu 135 Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His 215 Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala 235 His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro 245 250

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<220>

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<222> (101)..(979)

<223> RXN01631

<400> 481

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								gcg Ala									163
αa	ıt	ctc	agc	agc	cca	gta	σca	atc	gat	gag	cac	atc	act	cta	atc	act	211

gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala 25 30 35

gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259 Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys 40 45 50

gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307 Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala

gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355 Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala 70 75 80 85

act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403 Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe 90 95 100

gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451 Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly 105 110 115

gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499 Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe 120 125 130

act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547 Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu 135 140 145 BGI-126CP - 690 -

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gac gcc ggt tgg Asp Ala Gly Trp			_		883
cac cga agc ctc His Arg Ser Leu 265	Pro Val Lys			e Asp Thr	931
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Ala Asp Leu Ile 50	Lys Ala Arg 55		Gly Tyr Glu Gl 60	u Leu Arg	

Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu 65 70 75 80

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Lys	Val	Gly 115	Ala	Gly	Glu	Gly	Thr 120	Asn	Gly	Val	Val	Pro 125	Ile	Ala	His	
Met	Ala 130	Ser	Ala	Phe	Thr	Asp 135	Leu	Ala	Ala	Glu	Ala 140	Glu	Ala	His	Gly	
Val 145	Lys	Leu	Ala	Leu	Glu 150	Ala	Thr	Pro	Phe	Ser 155	His	Leu	Lys	Thr	Ile 160	
Tyr	Asp	Ala	Leu	Glu 165	Val	Val	Ser	His	Ser 170	Asp	Ser	Pro	Ser	Ala 175	Gly	
Leu	Met	Val	Asp 180	Ile	Trp	His	Thr	Ala 185	Lys	Ile	Gly	Ile	Pro 190	Asn	Asp	
Glu	Leu	Trp 195	Arg	Asn	Ile	Pro	Leu 200	Ser	Lys	Val	Asn	Ala 205	Val	Glu	Val	
Asp	Asp 210	Gly	Phe	Ile	Asp	Thr 215	Pro	Ile	Asp	Leu	Phe 220	Asp	Asp	Ser	Thr	
Asn 225	Arg	Arg	Ala	Tyr	Cys 230	Gly	Glu	Gly	Glu	Phe 235	Asp	Pro	Ala	Ser	Phe 240	
Ile	Arg	Gly	Ala	Ile 245	Asp	Ala	Gly	Trp	Thr 250	Gly	Ala	Tyr	Gly	Val 255	Glu	
Ile	Ile	Ser	Ala 260	Glu	His	Arg	Ser	Leu 265	Pro	Val	Lys	Glu	Gly 270	Leu	Gln	
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							gtg Val									163

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977

990

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Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala 50 55 60
Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val 65 70 75 80
Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser 85 90 95
Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn 100 105 110
Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly 115 · 120 125
Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser 130 135 140
Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu 145 150 155 160
Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile 165 170 175
Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly 180 185 190
Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro 195 200 205
His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg 210 215 220
Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg

225 230 235 240 His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser 245 250 Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr 260 265 Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp 280 Trp <210> 485 <211> 1173 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1150) <223> RXN00337 <400> 485 ggacgettat tggtgageat teggattaeg eeggtggtgt ggtgetggeg getaatgega 60 attgccggac tgcggctgcc gtcaataaag aaccgcgacg atg ttg tta acg tat 115 Met Leu Leu Thr Tyr 1 gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act 163 Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt 211 Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gcc 259 Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala 40 cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg 307 Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser 55 60 cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag 355 Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu 75 ggg gtg ggg ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg 403 Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu 95 gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att 451 Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile 110 gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg 499

Ala	Glu	Ile 120	Cys	Ser	Gln	Ser	Ala 125	Phe	Met	Phe	Ser	Glu 130	Thr	Ser	Val.	
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					ggt Gly											643
-		_	_	_	att Ile		_				_	_				691
	_	-	_		cgc Arg	-		_		_		_		_		739
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					aac Asn											883
					agg Arg											931
					agc Ser											979
					tgc Cys											1027
					gtg Val 315											1075
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cct																1173

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<211> 350

<212> PRT

<213> Corynebacterium glutamicum

<400> 486

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Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu
35 40 45

Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His 50 55 60

Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu 65 70 75 80

Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp 85 90 95

Val Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro 100 105 110

Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe 115 120 125

Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly 130 135 140

Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr 145 150 155 160

Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val 165 170 175

Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr 180 185 190

Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu 195 200 205

Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu 210 215 220

Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu 225 230 235 240

Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala 245 250 255

Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser 260 265 270

Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe 275 280 285

Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala 290 295 300

Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp 305 310 315 320

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<212> DNA

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<220>

<221> CDS

<222> (101)..(1225)

<223> RXS00584

<400> 487

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agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163 Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211 Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr 25 30 35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
40 45 50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307 Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355 Arg Leu Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala 70 75 80 85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403 Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp 90 95 100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451 Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr 105 110 115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
120 125 130

				gag Glu												547
				gat Asp												595
				tac Tyr 170												643
_			-	tct Ser	_			_	_	_	_			_		691
_				ttc Phe	_				-				_	_	_	739
_	_		_	cag Gln	_	_	_							, ,		787
				gcg Ala	_	_	-				_			_		835
				ttg Leu 250												883
				gcc Ala												931
				tcc Ser										-	_	979
				cgt Arg												1027
				atc Ile												1075
aac Asn	ctt Leu	gat Asp	cct Pro	gcg Ala 330	aaa Lys	ttg Leu	cgc Arg	atc Ile	aat Asn 335	Gly	ggt Gly	gaa Glu	ggc Gly	ctg Leu 340	gtg Val	1123
				gtg Val												1171
				gag Glu												1219

gcc aag taattaaggg cgctagactg tta
Ala Lys
 375

1248

<210> 488

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu

1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
35 40 45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe
50 55 60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Gly Pro Cys Ser Val 65 70 75 80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu 85 90 95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe 100 105 110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro 115 120 125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg 130 135 140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu 145 150 155 160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp 165 170 175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu 180 185 190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly 195 200 205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Gln Asn Pro His 210 215 220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr 225 230 235 240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly 245 250 255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly 260 265 270

Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys 280 Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu 305 315 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly 330 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp 340 345 Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg 360 Glu Arg Arg Ala Ala Lys 370 <210> 489 <211> 1131 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1108) <223> RXS02574 <400> 489 tgtgctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttatc 60 gacgtccccc tccacccctc ccgcaccgac cgcggaggat ttg gcg cgc gcg caa 115 Leu Ala Arg Ala Gln 1 atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly 10 gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly 25 ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro 40 45 ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser 60 gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile 75

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg

403

Leu	Gly	Asp	Phe	Pro 90	Ser	Pro	Arg	Val	Met 95	Ala	Gln	Thr	Met	Thr 100	Pro	
-		_	_	_		_	_							gct Ala	_	451
				_			-		_	_	_	_	_	gct Ala		499
						_	_							gcc Ala	_	547
														gta Val		595
			_									_	-	agt Ser 180		643
														ctt Leu		691
		_							-			-		gac Asp		739
														gac Asp		787
														agt Ser		835
_								_						gac Asp 260	_	883
								-					-	gaa Glu	-	931
		_				-		_	_		-			atc Ile	_	979
														gtt Val		1027
														aga Arg		1075
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ccc 1131

<210> 490

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser 1 5 10 15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu 20 25 30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val 115 120 125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser 130 135 140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
145 150 155 160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
165 170 175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala 180 185 190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
195 200 205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly 210 215 220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln 225 230 235

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val 245 250 255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His 260 265 270

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln 275 280 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys 325 330 335

<210> 491

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1008)

<223> RXS03215

<400> 491

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Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro 20 25 30

ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc  $\,$  144 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  $\,$  35  $\,$  40  $\,$  45

cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
50 60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu 65 70 75 80

ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga  $\phantom{0}$  288 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  $\phantom{0}$  85  $\phantom{0}$  90  $\phantom{0}$  95

tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc 336 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly 100 105 110

tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu 115 120 125

ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432

BGI-126CP - 704 -

Phe Val Ala 130	Gly Ser Asp	Phe Ala Ala 135	Val Arg Gly 140	Gly Gln Leu	Ser
		ccc aag cca Pro Lys Pro			
		gat gaa tac Asp Glu Tyr			
		tcc ttc atc Ser Phe Ile 185			
	Arg Ile Ser	cag gga cac Gln Gly His 200			_
		tcc gtg ctc Ser Val Leu 215	-	-	
		cca gca acc Pro Ala Thr			
	-	acc atc gga Thr Ile Gly	_		-
		gca cca ggc Ala Pro Gly 265			
	Phe Gln Ala	cgc gca ttc Arg Ala Phe 280			
		cca cgc tgc Pro Arg Cys 295	Ala Thr Leu		
		gat gct gta Asp Ala Val			
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<210> 492

<211> 336

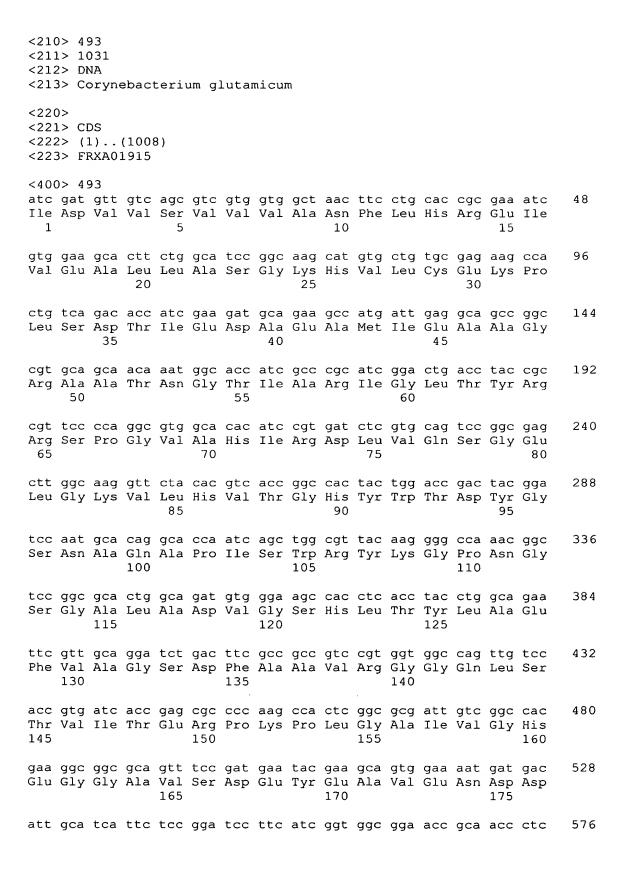
<212> PRT

<213> Corynebacterium glutamicum

<400> 492

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					4					•			; •	•		
Ile	Ala	Ser	Phe 180	Ser	Gly	Ser	Phe	Ile 185	Gly	Gly	Gly	Thr	Ala 190	Thr	Leu	
_	_	_	-			-					acc Thr				_	624
		_	_	_						_	ttc Phe 220	_				672
_							_				gac Asp		_		_	720
-			_							_	cac His				_	768
			_	_	_	_					att Ile				_	816
		_		-		_	_			-	gaa Glu		_			864
											ttg Leu 300	-	_			912
											tca Ser					960
			_		_			_	_	_	atc Ile		_			1008
taga	aact	at t	caga	aaago	ca to	ca										1031
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	)> 49 Asp		Val	Ser 5	Val	Val	Val	Ala	Asn 10	Phe	Leu	His	Arg	Glu 15	Ile	
Val	Glu	Ala	Leu 20	Leu	Ala	Ser	Gly	Lys 25	His	Val	Leu	Cys	Glu 30	Lys	Pro	
Leu	Ser	Asp 35	Thr	Ile	Glu	Asp	Ala 40	Glu	Ala	Met	Ile	Glu 45	Ala	Ala	Gly	
Arg	Ala 50	Ala	Thr	Asn	Gly	Thr 55	Ile	Ala	Arg	Ile	Gly 60	Leu	Thr	Tyr	Arg	

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu

- 708 -70 75 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly

80

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly 105

Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu 120

Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gln Leu Ser 130 135

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His 155

Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp 165

Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu 195

Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly

Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu 235

Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu

Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile 280

Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu

His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Gly 315

Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn 325 330

<210> 495

<211> 1288

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258) <223> RXS03224

<400> 495

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gcc a																787
act f Thr 1 230																835
ttc a																883
tca a Ser i				_	_	_						_				931
cca a																979
gat a		-			_	_	-							_		1027
ttt : Phe : 310			_					_				_	-			1075
gcg (																1123
ctt ( Leu (																1171
ggt ( Gly (																1219
atc ( Ile !		_			_		_		-		_	_	_	tgto	egg	1268
ttcaa	aggg	gta ç	gggga	acaa	aa											1288
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Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly

35

40

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly 50 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu 65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly 85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Lys Tyr 100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala  $\cdot 115$  120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val 130 135 140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala 145 150 155 160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val 165 170 175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly 180 185 190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
195 200 205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe 210 215 220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr 225 230 235 240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala 245 . 250 . 255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ile Leu Phe 260 265 270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe 275 280 285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro 290 295 300

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile 305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln 325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys 340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu 355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala 385 <210> 497 <211> 1281 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1258) <223> FRXA00038 <400> 497 acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60 tggaactcat tgaacgccgc gcccggctaa ggtgggaggc atg agt ttt gct gaa 115 Met Ser Phe Ala Glu 163 cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro 10 atc egg cet gaa gee eee gea eet gte aca eat egg ete eee aat eta 211 Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu 259 att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307 Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp 60 355 tte tac ege ate gae eeg ege ete gge ace gag gaa gae atg gae geg Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala 70 403 ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly 90

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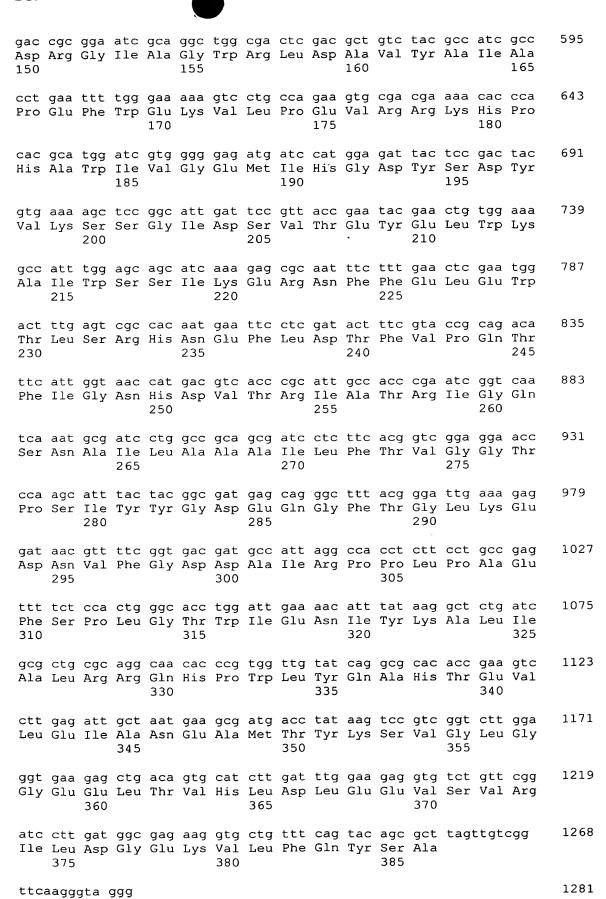
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gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc

Val Phe Asn His Val Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr

105

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547 Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu 135 140 145



<210> 498

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
1 5 10 15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His 20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly 35 40 45 .

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu 65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly 85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Lys Tyr 100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala 115 120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val 130 135 140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala 145 150 155 160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val 165 170 175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly 180 185 190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu 195 200 205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe 210 215 220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr 225 230 235 240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala 245 250 255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ile Leu Phe 260 265 270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe 275 280 285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro 290 295 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile 315 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln 325 330 335 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys 345 Ser Val Gly Leu Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu 355 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala 385 <210> 499 <211> 517 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(517) <223> RXC00233 <400> 499 cgcctccagc agttgaggga gaagttccaa cacttgcacc aactgaggaa gcaactgtgc 60 aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115 Met Ser Val Asn Glu 1 gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly 10 gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr tac ttq aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val 60 gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403 BGI-126CP - 716 -

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	gcg ctc agc Ala Leu Ser 10					
_	atc cct gaa Ile Pro Glu 25	Asp Val Pr				_
	gat aca gag Asp Thr Glu					
	gaa cca att Glu Pro Ile					
	tat gga aac Tyr Gly Asn 75			_		
	ctg ggg tgg Leu Gly Trp 90					
	ggt acc tac Gly Thr Tyr 105		's Met Phe			
	gga gtt gca Gly Val Ala					
	ggg ttt gcg Gly Phe Ala	-	-			
	act gaa tat Thr Glu Tyr 155					
	tgg cga ctt Trp Arg Leu 170					
	aac caa att Asn Gln Ile 185		a Ala Leu			
	aac gat cgt Asn Asp Arg					
	tct tac aac Ser Tyr Asn	_	_			_

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gat	gct	gcc	gcg	tcc	tac	gct	tta	cga	cag	ccg	gcg	atc	taaaacttaa	836
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Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$ 

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr 130 135 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro 225 230 235 240

Ala Ile

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                                             Met Phe Ser Ser Arg
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Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
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teg tge tea age gat tee agt gae age tee ace tee act gat get gea
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ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct
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Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
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Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
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                                     95
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Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
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                                                     115
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Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
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                            125
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Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
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                        140
tct gat atc gca ccg att gag cag ttg gag ctt ttg cag cag ctg
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Ser Asp Ile Ala Pro Ile Glu Gln Leu Glu Leu Leu Gln Gln Leu
150
                    155
                                         160
                                                             165
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Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
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		gtt gat gtc atc tac Val Asp Val Ile Tyr 225	
		tct tct ctg gtt cag Ser Ser Leu Val Gln 240	
Gln Lys Gln Ile P		gct gag tcc ggc act Ala Glu Ser Gly Thr 255	
	hr Leu Gly Ile A	gat tac acc gag ctt Asp Tyr Thr Glu Leu 270	,, ,
		ctg cag gac ggc gaa Leu Gln Asp Gly Glu 290	
		gag ttc acc tac gtg Glu Phe Thr Tyr Val 305	
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Ser Thr Asp Ala A	la Gly Gly Asp S 40	Ser Tyr Arg Val Gly 45	Ile Asn Gln
Leu Val Gln His P 50	ro Ala Leu Asp <i>F</i> 55	Ala Ala Thr Thr Gly 60	Phe Lys Glu

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Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala 80

Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser 90

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala 110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr 125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asp Ile Ala Pro Ile Glu Ala Pro Gly Gly 135

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu 160

Leu Leu Gln Gln Gln Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
180 185 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr 195 200 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val 210 215 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu 225 230 235 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser 245 250 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr 260 265 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp 275 280 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr 290 295 300

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Arg	Leu 215	Thr	Ser	Val	Leu	Arg 220	Glu	Ala	His	Pro	Tyr 225	Glu	Glu	Pro	Ala	
	gat Asp		_	-	_		_	_		_		-				835
	ttg Leu															883
	gtg Val			_	_			_		-		-				931
_	gct Ala			_		_		_			_			-		979
	ggg Gly 295	_		_	_				_			_				1027
	gtt Val															1075
	cga Arg	_				-	-		-		-			-	_	1123
_	ttt Phe						-		_		-	-	-		-	1171
	cag Gln	_	-	_	_			_		_		_				1219
_	tct Ser 375		_	_			taaa	attct	tg a	agaad	ctaaa	aa aa	ag			1263
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Tyr	Pro	Pro	Ala 20	Leu	Ala	Glu	Ser	Trp 25	Asp	Lys	Val	Gly	Leu 30	Ile	Cys	
Gly	Asp	Pro 35	Thr	Glu	Ser	Val	Lys 40	Arg	Val	Gly	Leu	Ala 45	Leu	Asp	Cys	
Thr	Gln 50	Ala	Val	Ala	Asp	Lys 55	Ala	Val	Asp	Met	Gly 60	Leu	Asp	Met	Leu	

100

Ile Ile His His His ProLeu Leu Leu Arg Gly Val Thr Ser Val Ala Ala 65Asp Glu ProLys Gly Lys Val Ile His Thr Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile 115 120 125

105

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu 130 135 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala 145 150 155 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr 165 170 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val 180 185 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro 195 200 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro 210 215 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser 225 230 235 240

Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro 245 250 255

Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val 260 265 270

Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser 275 280 285

Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val 290 295 300

Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His 305 310 315 320

Pro Val Asp Glu Tyr Leu Arg Glu Gly Pro Ala Val Ile Asp Thr 325 330 335

Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile 340 345 350

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                                            Met Gly Ile Ile Ala
ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa
                                                                   163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
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Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
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                                                                   259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
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Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
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ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc
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Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
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Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
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                                                                   451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
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                                110
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Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
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Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
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ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca
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Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
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                                        160
ttg cca gct gca gct tct tcg gcc tct cag gtg tac att gct ttg
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Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
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		-			att Ile 205							739
					aag Lys							787
			_		gta Val					_		835
					gtt Val							883
					att Ile							931
_	 _		_	-	aac Asn 285	_	-			_	-	979
	_	_	_		ttt Phe		_		_	_		1027
				Asn	atc Ile							1075
					tcc Ser							1123
					tgc Cys							1171
					att Ile 365							1219
					act Thr							1267
					tcc Ser							1315
					gca Ala							1363

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Val Gly Thr Al 35	a Leu Val	Gly Gly Val 40	Asn Ala Pro	Thr Leu Leu Ile 45
Asp Ala Val Va 50	l Asp Ala	Ala Gln Ser 55	Glu Val Thr 60	Phe Ala Gly Met
Ala Phe Val Ph 65	e Met Gly 70	Ile Val Val	Gln Ser Thr 75	Gly Leu Ile Asp 80
Arg Leu Ile Al	a Ile Leu 85	Asn Ser Ile	Phe Gly Arg 90	Leu Arg Gly Gly 95
Ala Gly Tyr Va 10		Leu Gly Ser 105	Ala Leu Ile	Gly Leu Ile Ala 110
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Trp Met Lys Ly 130	s Thr Gly	Trp Thr Ala 135	Glu Arg Ser 140	Ala Thr Leu Val
Ala Gly Asn Se 145	r Gly Leu 150	Gly Val Ala	Leu Pro Pro 155	Asn Ser Thr Met 160
Phe Ile Ile Le	u Ala Leu 165	Pro Ala Ala	Ala Ala Ser 170	Ser Ala Ser Gln 175
Val Tyr Ile Al 18		Cys Gly Gly 185	Ala Tyr Ala	Val Leu Tyr Arg 190
Leu Ala Val Va 195	l Phe Tyr	Trp Thr Arg 200	Lys Asp Lys	Ile Pro Ala Thr 205
Pro Asp Asp Gl 210	n Arg Val	Ser Phe Gly 215	Glu Ala Met 220	Lys Thr Gly Trp
Arg Ser Pro Le 225	u Ile Phe 230	Leu Gly Ile	Leu Ile Pro 235	Val Ile Leu Thr 240

1411

1457

1470

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						aat Asn										355
						gac Asp										403
						atc Ile										451
	-	-	_			gct Ala						-	_	_	-	499
_	_	_	_	_	_	gct Ala 140	_		_	_			_	_		547
		_		_		gac Asp								-	-	595
_			_	_	-	cgc Arg	_			_	-	_	_	_		643
						gcc Ala										691
						ctg Leu										739
						gtg Val 220										787
						gct Ala										835
tac	ggc	agc	gtc	tac	gag	gtg	ttc	tcc	aat	сса	caa	aca	cag	gtt	gct	883

Tyr Gly Ser	Val Tyr 250	Glu V	al Phe	Ser	Asn 255	Pro	Gln	Thr	Gln	Val 260	Ala	
caa aag ttc Gln Lys Phe		_						-			-	931
tcg gaa gat Ser Glu Asp 280	-	_			_	_				_	_	979
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ggt gct ttt Gly Ala Phe 310												1075
caa tca ttt Gln Ser Phe		_	_	_						-		1123
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Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg 130 135 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn 145 150 155 160

Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala 165 170 175

Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr 180 185 190

Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg 195 200 205

Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu 210 215 220

Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser 225 230 235 240

Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro 245 250 255

Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr 260 265 270

Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu 275 280 285

Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala 290 295 300

Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val 305 310 315 320

Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr 325 330 335

Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr 340 345 350

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											Met 1	Ser	Leu	Ile	Glu 5	
						acc Thr										163
						gat Asp							-			211
						ggc Gly										259
		_	_	-	_	cca Pro 60		-		_			_	_		307
						agc Ser										355
	-					ttt Phe	_				_					403
		_	_			gaa Glu	_		_	_					_	451
						cgt Arg										499
						cat His 140										547
						gct Ala	Arg	Ala		Ala	Asn					595
						act Thr										643
						cac His										691
	-					aac Asn				-	-	_		_		739
						ggg Gly 220										787
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230

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<213> Corynebacterium glutamicum

<400> 512

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Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser 35 40 45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr 50 55 60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu 65 70 75 80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn 85 90 95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met 100 105 110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu 115 120 125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu 130 135 140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala 145 150 155 160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp 165 170 175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys 180 185 190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala 195 200 205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly 210 215 220

Ser Glu Val Lys His Ser 225 230

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	20	00				205					210				
cag co Gln Ar 21	-		_	_	_			_	_		_		_	_	787
ctg go Leu Al 230	-					-		_		_	_		-	_	835
gtc co Val A		-							-			_	-		883
tcc ta Ser Ty			Tyr												931
gat co Asp Pr		u Met													979
cct to Pro Le															1027
ttt at Phe Me 310															1075
gag ct Glu Le						-		_			_	_			1123
ggc ac Gly Th												taga	aaata	agt	1172
aactg	tgttg	gac													1185
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Asp Aı		u Asp	Ser	Leu	Val	Ser 40	Gln	Gly	Lys	Lys	Gly 45	Ala	Glu	Lys	
Val Le	eu Ty 50	r Ala	Thr	Glu	His 55	Leu	Ser	Ile	Met	Leu 60	Ala	Gly	Ala	Gln	
Phe GI 65	ly Il	e Thr	Val	Cys 70	Ser	Leu	Ile	Leu	Gly 75	Lys	Val	Ala	Glu	Pro 80	

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro 85 90 95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile 100 105 110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala 115 120 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile 130 135 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile 145 150 155 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu 165 170 175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser 180 185 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
195 200 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp 210 215 220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His 225 230 235 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val 245 250 255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile 260 265 270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro 275 280 285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met 290 295 300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln 305 310 315 320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu 325 330 335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser 340 345 350

Asp Asp

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732

Glu Asn Pro Gln Phe Asp 200

<210> 516

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

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Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg 35 40 45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro 50 55 60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly 65 70 75 80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly 85 90 95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu 100 105 110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp 115 120 125

Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly 130 135 140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe 145 150 155 160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile 165 170 175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Glu Ile 180 185 190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp 195 200

<210> 517

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXC01021

<400> 517

- 739 -

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Trp	Ala 50	Arg	Thr	Ala	Val	Glu 55	Gln	Leu	Ser	Glu	Arg 60	Arg	Ala	Glu	Ile	
Asn 65	Ala	Leu	Asn	Val	Phe 70	Pro	Val	Pro	Asp	Ala 75	Asp	Thr	Gly	Ser	Asn 80	
Met	Thr	Tyr	Thr	Met 85	Thr	Ala	Ala	Leu	Asp 90	Glu	Ala	Leu	Lys	Leu 95	Gly	
Glu	Leu	Gly	Asp 100	Val	Ala	Arg	Ile	Thr 105	Glu	Ala	Leu	Ala	Val 110	Gly	Ser	
Val	Arg	Gly 115	Ala	Arg	Gly	Asn	Ser 120	Gly	Val	Val	Leu	Ser 125	Gln	Val	Leu	
Arg	Ala 130	Ile	Ala	Gln	Ala	Ala 135	Ala	Asp	Gly	Val	Ile 140	Asp	Gly	His	Thr	
Ile 145	Gln	Glu	Ala	Leu	Ser 150	Ile	Ala	Arg	Ser	Leu 155	Val	Asp	Arg	Ala	Ile 160	
Thr	Asp	Pro	Val	Glu 165	Gly	Thr	Val	Val	Thr 170	Val	Leu	Arg	Ser			
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cata	atggo	ctc t	acca	gcgo	cc aa	atgco	gaagt	ago	gaaga	att	_		atg Met		_	115
								ctc Leu						-		163
					_			cat His 30	_	_	-		-	_		211
								ggc Gly								259
								tcc Ser								307

55 60 65 ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat 451 Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp 105 110 gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly 120 gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc qca ctq Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu 135 140 ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc 595 Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu 150 155 gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa 643 Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Asp Leu Lys 170 cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc 691 Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala 185 gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca 739 Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala 200 gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc 787 Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile 220 agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg 835 Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly 230 235 get gaa ate ate ege gae aac aac eac gte ege ate gee ace ace ace 883 Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr 250 ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg 931 Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly 265 270 atc gcg ctg gaa ggc ttc gct qca aaa ccc gcc acc ttg gaa tcc gta Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val tte atg gae ate gee tea ete gag aac ace teg etg caa ace gee 1024 Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala 300

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<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 520

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20 25 30

Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr 35 40 45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr 50 55 60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg 65 70 75 80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu 85 90 95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro 100 105 110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu 115 120 125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp 130 135 140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu 145 150 155 160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu 165 170 175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His 180 185 190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn 195 200 205

Ala Gly Glu Ile Ala 'Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg 210 215 220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu 225 230 235 240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg 245 250 255

Ile Ala Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp 260 265 270

Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala 275 280 285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser 290 295 300

Leu Gln Thr Ala 305

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<211> 1131

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1108)

<223> RXC01306

<400> 521

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	•			Met	Thr	Glu	Trp	Tyr	
				1				5	

gtc	gtt	tta	ccc	gcc	act	att	cta	ctc	atc	gcg	ctg	tct	gcg	ttt	ttc	163
Val	Val	Leu	Pro	Ala	Thr	Ile	Leu	Leu	Ile	Ala	Leu	Ser	Ala	Phe	Phe	
				10					15					20		

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gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
40 45 50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg 307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
55 60 65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct 355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
70 75 80 85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat 403 Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp 90 95 100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451 Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu 105 110 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag 499 Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu 120 125 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg 547 Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu

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Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro 85 90 95

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Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg 130 135 140

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Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His 180 185 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser 195 200 205

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His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser 260 265 270

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cgt t Arg (	_		-			-		_		-	-	_				163
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act o																307
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110

105

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Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu 65 70 75 80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro 85 90 95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu 100 105 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val 115 120 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu 130 135 140

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tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259 Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Pro Asp Pro Glu

307 ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag 355 Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu 70

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat 403 Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp

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					caa Gln									-		691
			_		aac Asn		_	Ile						_	_	739
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Arg Lys Val Arg Th		Leu Pro Ser 3	Leu Glu Gln	Asn Ile 95
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Gln Gly Val Ala Il 180	e Gly Ala Cys	Leu Glu Ile 7	Ala Leu Lys 190	Leu Arg
Glu Arg Ala Gly Le 195	u Thr Thr Thr 200		His Trp Ser . 205	Asp Ala

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly Asp Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr 265 Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe 290 295 300 Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu 305 310 Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu 325 Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala 340 Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg 370 <210> 535 <211> 800 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(777) <223> RXC02254 <400> 535 atc gcc gtt gcc gaa gaa ggc gga ttg tgg gaa aac ctc ctg cag cac 48 Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His ege tte ggt gga cat ggt geg eta get ggt cae gee ttg gga aac ete Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu 20 gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt 144 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu 35 gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta 192 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val

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		ccc Pro 115														384
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		atc Ile														480
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Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val 50 55 60

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser 65 70 75 80

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala 85 90 95

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu 100 105 110

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr \$115\$ \$120\$ \$125\$

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val 130 135 140

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val 145 150 155 160

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala 165 170 175

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val 180 185 190

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg 195 200 205

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe 210 215 220

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His 225 230 235 240

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Arg Lys Arg

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agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His 230 235 240 245	835
ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu 250 255 260	883
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Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg 1 10	
Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg 10  Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala 20  Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln 40  Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val	
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Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg 15  Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala 25  Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln 45  Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val 50  Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Asp Asn Ala Asp 65  Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val Uys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu	
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Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala 165 Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu 185 Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly 195 200 205 Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala 215 Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp 225 230 Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val 295 Thr Glu Asp Leu Leu Glu Glu Ile 305 310 <210> 539 <211> 681 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(658) <223> RXC02435 <400> 539 tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tctttagcca 60 tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg 115 Val Thr Asp Asn Leu ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met 10 gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu 25 cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu 45 40 50

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								gct Ala								403
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_						_		aac Asn		_			_	_		499
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Ala	Val	Ile	Trp	Met 85	Asp	Pro	Tyr	Ser	Pro 90	Thr	Ala	Gly	Ala	Ser 95	Gly	

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Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala 115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly 130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr 145 150 155 160

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Val Thr Asp Asn Leu

1 5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg  $\,$  163 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met  $\,$  10  $\,$  15  $\,$  20

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cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu 40 45 50

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atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met

gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met 90 95 100

atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451

Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg 105 110 115	
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Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly 130 135 140	
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tte tgg ege gag ace gae ege tte gee gea gat eae gge gtg aaa gtg

Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp His Gly Val Lys Val

595

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	gct cag ctc aac ggt Ala Gln Leu Asn Gly 235		
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	gaa ggc gtc aac gaa Glu Gly Val Asn Glu 315		
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                                             Val Ala Thr Asp Asn
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Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
atc gag gct tct gag ggt aac aac ggt gtt gtc ctg ggc aag atg ctg
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Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
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Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly
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Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
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Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe
70
aac gag gtt tet tac eta ett ate aac ggt gag eta eea ace eea gat
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Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp
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	g tcc ı Ser			_				_		_	-	-	-		_	931
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	a ggc a Gly															1363
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cgt 1416

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<400> 546

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Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly 35 40 45

Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly 50 55 60

Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala 65 70 75 80

Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu 85 90 95

Leu Pro Thr Pro Asp Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
100 105 110

His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro 115 120 125

Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu 130 135 140

Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu 145 150 155 160

Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala 165 170 175

Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn 180 185 190

Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro

Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys 210 215 220

Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr 225 230 235 240

Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala 245 250 255

Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln

			260					265					270			
Ala	Val	Leu 275	Glu	Met	Leu	Glu	Asp 280	Ile	Lys	Ser	Asn	His 285	Gly	Gly	Asp	
Ala	Thr 290	Glu	Phe	Met	Asn	Lys 295	Val	Lys	Asn	Lys	Glu 300	Asp	Gly	Val	Arg	
Leu 305	Met	Gly	Phe	Gly	His 310	Arg	Val	Tyr	Lys	Asn 315	Tyr	Asp	Pro	Arg	Ala 320	
Ala	Ile	Val	Lys	Glu 325	Thr	Ala	His	Glu	Ile 330	Leu	Glu	His	Leu	Gly 335	Gly	
Asp	Asp	Leu	Leu 340	Asp	Leu	Ala	Ile	Lys 345	Leu	Glu	Glu	Ile	Ala 350	Leu	Ala	
Asp	Asp	Tyr 355	Phe	Ile	Ser	Arg	Lys 360	Leu	Tyr	Pro	Asn	Val 365	Asp	Phe	Tyr	
Thr	Gly 370	Leu	Ile	Tyr	Arg	Ala 375	Met	Gly	Phe	Pro	Thr 380	Asp	Phe	Phe	Thr	
Val 385	Leu	Phe	Ala	Ile	Gly 390	Arg	Leu	Pro	Gly	Trp 395	Ile	Ala	His	Tyr	Arg 400	
Glu	Gln	Leu	Gly	Ala 405	Ala	Gly	Asn	Lys	Ile 410	Asn	Arg	Pro	Arg	Gln 415	Val	
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gcaç	gacca	ata a	aggto	ctgc	et tt	tcg	cgtat	taa	atgaç	gtac	-		_	ctt Leu		115
							gca Ala									163
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						gcg Ala									499
						cac His 140									547
_		_				gaa Glu			_	_		_			595
						ctc Leu									643
						gat Asp									691
		_	-	_		cgg Arg			_			_	_		739
						att Ile 220									787
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Ile Asp Leu Glu Asp Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr 35 40 45

Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg 50 55 60

Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg 145 150 155 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala 165 170 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu 180 185 190

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala 195 200 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala 210 215 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu 225 230 235 240

Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile 245 250 255

Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro 260 265 270

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                                                                   115
                                            Met Ala Lys Ile Ile
tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag
                                                                   163
Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys
                 10
ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc
                                                                   211
Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr
                                                                   259
cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc
Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg
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ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag
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Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu
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                                                                   355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser
gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag
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Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln
gge tac gac atc cca gaa ctg cct gat aac gcc acc gac gag gaa
Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu
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Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn
cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc
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Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val
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Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala
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                                        160
gat tee aag ace aac gtt gea ace atg gat gea aac gae tte ege eac
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Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His
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aac gag aag too ato ato oto gac got got gat gaa gtt cag ato aag
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		_		_	gtt Val		_			_	_		_	_	-	787
_	_	_			ctc Leu 235		_	-	-		-	_	_	-		835
				_	cac His	_	_	_		_		-	_		_	883
					cac His				-			-	_	_		931
_	_				cag Gln	_		_	_					_		979
					ctc Leu											1027
					ttc Phe 315											1075
					gct Ala											1123
			Val	Asp	gct Ala	Ser	Met	${\tt Pro}$	Āla					Ser		1171
					gac Asp											1219
					gct Ala											1267
					ttc Phe 395											1315
					cag Gln											1363
					gca Ala											1411

425 430 435 ggc gac gtt ctc atc gag cac gac gtt gag gca aat gac atc tgg cgt Gly Asp Val Leu Ile Glu His Asp Val Glu Ala Asn Asp Ile Trp Arg 445 gca tgc cag gtc aag gat gcc cca atc cag gat tgg gta aag ctt gct 1507 Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala 455 460 gtc acc cgc tcc cgt ctc tcc gga atg cct gca gtg ttc tgg ttg gat 1555 Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp 470 475 cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac 1603 Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr 490 ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct 1651 Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro 505 gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac 1699 Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp 520 acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc 1747 Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu 535 ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt 1795 Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val 550 cet ttg atg get gge gga etg tte gag ace ggt get gga tet 1843 Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser 570 gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg 1891 Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp gat tee ete ggt gag tte ete gea etg get gag tee tte ege eac gag 1939 Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu 605 ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg 1987 Leu Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu 615 gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc 2035 Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag 2083 Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys 655 ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct 2131 Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala 670

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	Leu	Pro	Asn	Ile	Ser 85	Ala	Ser	Val	Pro	Gln 90	Leu	Lys	Ala	Ala	Ile 95	Lys	
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i	Asn	Asp	Phe	Arg 180	His	Asn	Glu	Lys	Ser 185	Ile	Ile	Leu	Asp	Ala 190	Ala	Asp	

Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu 195  $\phantom{\bigg|}200\phantom{\bigg|}205\phantom{\bigg|}$ 

Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val 210 215 220

Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg 225 230 235 240

Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met 245 250 255

Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr 260 265 270

Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly 275 280 285

Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser 290 295 300

Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu 305 310 315 320

Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn 325 330 335

Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met 340 345 350

Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp 355 360 365

Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr 370 375 380

Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met 385 390 395 400

Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr 405 410 415

Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln
420 425 430

Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala 435 440 445

Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp 450 455 460

Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala 465 470 475 480

Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser 485 490 495

Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile 500 505 510 Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile 515 520 525

Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp 530 540

Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys 545 550 555 560

Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr 565 570 575

Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu 580 585 590

Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu 595 600 605

Ser Phe Arg His Glu Leu Asn Asn Gly Asn Thr Lys Ala Gly Val 610 620

Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu 625 630 635 640

Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His 645 650 655

Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu 660 665 670

Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn 675 680 685

Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly 690 695 700

Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr 705 710 715 720

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Lys Lys

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<211> 1059

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<222> (1)..(1059)

<223> FRXA00521

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							cca Pro									432
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							gca Ala									576
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							tcc Ser									768
cac	gac	gtt	gag	gca	aat	gac	atc	tgg	cgt	gca	tgc	cag	gtc	aag	gat	816

130

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135

140

Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp 165 170 Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala 185 Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe 195 200 Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln 215 Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala 225 230 Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp 295 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr 305 310 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly

Asn

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cgc Arg 50														192
gac Asp														240
ggc Gly										-	_			288
ggt Gly					-			_	-	_		_		336
acc Thr	_									_			-	384
 ctg Leu 130	_	_	-	_	-	_	_			_		_		432
gtt Val										-	-			480
cag Gln		-			_	_			_	-				528
tcc Ser														576
gag Glu														624
gtt Val 210														672
aag Lys														720
gct Ala														768
cag Gln														816

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				gca Ala												912
				acc Thr												960
				gca Ala 325												1008
				atc Ile												1056
	_			gac Asp					_				_			1104
				cag Gln												1152
			_	ggt Gly			-					-	_	_	_	1200
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		_	_	tcc Ser	_			_	_	_			_	_	-	1344
				aag Lys												1392
				aac Asn												1440
				cac His 485												1488
				gca Ala												1536
acc	gag	acc	ttc	gac	atc	acc	gga	ctg	acc	gca	ctt	aac	gag	ggc	gag	1584

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Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu 50 55 60

Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala 65 70 75 80

Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro 85 90 95

Gln Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser 100 105 110

Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala 115 120 125

Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro 130 135 140

Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr 145 150 155 160

Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr 165 170 175

Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu 180 185 190

Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr 195 200 205

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Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro 485

Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly 500

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	cca Pro	_		_	_		_			_				_		499
	cgc Arg 135															547
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	ttc Phe	_	_	_							_		_	_		643
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Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val 115 120 125

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Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly 145 150 155 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile 165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn 180 185 190

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Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg 35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala 50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro 65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp 85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn 100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val 115 120 125

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Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
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Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile 165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn 180 185 190

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										ggc Gly						576
										cag Gln						624
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					cac His											864
					gca Ala											912
					ggt Gly 310											960
					ctg Leu											1008
					ccg Pro									-		1056
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					gac Asp											1296
					ggc Gly											1344
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ttc act gag Phe Thr Glu				Val							2496
gca gat gca Ala Asp Ala 835										-	2544
tac tac gaa Tyr Tyr Glu 850											2592
gcg atc gtt Ala Ile Val 865	Arg Ile (										2640
tcc gag gct Ser Glu Ala			Pro Asr	_	Glu		-			_	2688
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ctc cca gag Leu Pro Glu 915		Pro Asn									2784
cgc gct cag Arg Ala Gln 930											2832
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Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr 35 40 45

Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg 50 55 60

Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe 65 70 75 80

Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val 85 90 95

Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu 100 105 110

Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser 115 120 125

Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile 130 135 140

Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val 145 150 155 160

Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser 165 170 175

Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His 180 185 190

Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala 195 200 205

Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys 210 215 220

Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val 225 230 235 240

Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu 245 250 255

Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val 260 265 270

Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile 275 280 285 •

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600

Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu

- 805 -

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Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala

945 <210> 563 <211> 1517 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1494) <223> RXA01745 <400> 563 ate ett gea gae gae gae gee gte gae gte gge gea gte ate gee 48 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Ala 20 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144 Ala Pro Ala Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu 35 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu 50 atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg 240 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp 65 ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag 288 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu 8.5 gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc 336 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly 100 105 acc atc gtg gag atc ctt gca gac gac gac gac acc gtc gac gtc ggc 384 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly 115 120 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala 135 gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag 480 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Pro Val Lys Glu Glu 155 528 Pro Lys Lys Glu Glu Pro Lys Lys Glu Pro Lys Lys Glu Ala Ala 165 170 act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac 576

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Thr	Thr	Pro	Ala 180	Ala	Ala	Ser	Ala	Thr 185	Val	Ser	Ala	Ser	Gly 190	Asp	Asn	
-			gtc		cca Pro	_		cgc	_		-	_	aag			624
_	_	_			gtg Val								_		_	672
					gct Ala 230											720
					tcc Ser											768
					ggt Gly											816
					acc Thr											864
					gtc Val									-	-	912
_		_			ttc Phe 310			_								960
					aag Lys											1008
				Ser	ttc Phe	Asn		Lys	Thr					Tyr		1056
		-			tcc Ser		_	_	_			_		_	_	1104
		-			gat Asp	-	_	_							_	1152
					ctg Leu 390											1200
		_			ggt Gly											1248
					gat Asp											1296

420 425 430 ato ttg ggc acc ggc gcg atc gtg aag cgt cca gtt gtc atc acc gag 1344 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu 435 440 gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg 1392 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu 450 455 ace tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg 1440 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg 1488 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu 490 1517 cag ctc taagatctct gcaagttaaa acc Gln Leu <210> 564 <211> 498 <212> PRT <213> Corynebacterium glutamicum <400> 564 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Ala Ala Pro Ala Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu 40 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly 105 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Aro Ala 135 140 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu 145 150 155 Pro Lys Lys Glu Glu Pro Lys Lys Glu Pro Lys Lys Glu Ala Ala 165 170

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn 185 Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg 210 215 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu 225 230 235 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu 245 250 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr 315 Leu Pro Phe Phe Val Lys Ala Val Glu Ala Leu Val Ser His Pro Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His 345 Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser 410 Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly 425 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu 450 455 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu 470 475

Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu

490

485

Gln Leu

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gttcgcaacc gctaatt	agt taaggagcac	Me	g tct att ttt t Ser Ile Phe 1	
aat tca gat tcc cg Asn Ser Asp Ser Ar 1	g Ile Ile Ile G			
tca gag cat gcg cg Ser Glu His Ala Ar 25				
ggc acc aac ccc cg Gly Thr Asn Pro Ar 40				
gag ttg cct gta tt Glu Leu Pro Val Ph 55		ys Glu Ala Me		
gcg gat gtc acc gt Ala Asp Val Thr Va 70	_	_		
atc att gaa gct at Ile Ile Glu Ala Il 9	e Asp Ala His I			
gag ggc atc cca gt Glu Gly Ile Pro Va 105	l Arg Asp Ala S			
aag gtg gga cac ac Lys Val Gly His Th 120				
act ccc ggc gaa tc Thr Pro Gly Glu Se 135			a Asn Ile Ala	
tcc ggc ccg atc gg Ser Gly Pro Ile Gl 150				

_	_	tac Tyr	-			_					_					643
		gac Asp									_	-	_		-	691
	_	gct Ala 200	_				_	_		_	_					739
		gat Asp														787
		cca Pro	-					-				-		_		835
		atg Met														883
	_	gca Ala	_	_		_	_		_			_	_			931
		ccg Pro 280														979
ttg Leu	taad	ctaad	cag (	gcca	cagat	ic t	ī.a									1005

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<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

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Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly 20 25 30

Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile

Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala 50 55 60

Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala 65 70 75 80

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu 85 90 95

- 813 -BGI-126CP Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn 120 Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro 135 Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly 150 145 155 Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser 165 170 Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile 180 185 Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala Leu 290 <210> 567 <211> 1395 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1372) <223> RXA00783 <400> 567 aaagttccca aggggtgggg gctgagcacc acggatccaa ttttgttgca atttgcaaag 60

tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt 115 Leu Lys His Leu Leu 1 5

tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg  $\,$  163 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro  $\,$  10  $\,$  15  $\,$  20

_	_	_	_	gca Ala		_			_			-		_		211
				ggt Gly												259
				agg Arg												307
				gtc Val												355
_		-	_	acg Thr 90	_	_	_	_		_	-		_			403
		_	-	atc Ile												451
		-	-	att Ile	-	-										499
				tcg Ser												547
				ctg Leu												595
				ctc Leu 170												643
				ggc Gly												691
	-		_	atc Ile		_				_		-	_			739
				ccg Pro												787
	_		_	atc Ile	_	_	-	_		_	-		_		-	835
				ttg Leu 250												883
ctg	aag	gcc	aag	aag	aat	gat	ctg	aac	tac	gtg	aaa	ctt	gat	ggc	tct	931

Leu	Lys	Ala	Lys 265	Lys	Asn	Asp	Leu	Asn 270	Tyr	Val	Lys	Leu	Asp 275	Gly	Ser	
						ggt Gly										979
		_	_	_		gaa Glu 300	_				_	_				1027
						gga Gly										1075
						gat Asp										1123
						gcg Ala										1171
	-	-	_			ggc Gly	_		-	_	_					1219
						gtg Val 380										1267
				_	-	acc Thr	_				_	_	_		_	1315
_		_	_			gcc Ala			-	_			_		_	1363
	gct Ala		tagt	taaç	gga ç	gcaco	ctgtt	t aa	at							1395

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<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

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Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr 20 25 30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile 50 55 60

Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn 105 Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe 120 Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser 130 135 Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp 215 Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala 225 Asp Phe Arg His Asp Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly 295 Gln Arg Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu

Ser Met Ala Ala Gly Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg 335

Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val 340

Ala Lys Gly Ile Val Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr

Lys Pro Leu Val Val Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg 370 375 380

360

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Arg Ile Leu Ala Glu Tyr Asn His Pro Leu Val Thr Val Val Glu Gly 385 390 395 400

Met Asp Ala Ala Asp His Ala Ala His Leu Ala Asn Leu Ala Gln
405 410 415

His Gly Gln Phe Ala Thr Ala Asn 420

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<211> 1623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1600)

<223> RXN01695

<400> 569

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				Met	Ser	Asp	Ser	Pro	
				1		_		5	

- aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163 Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly 10 15 20
- gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211
  Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu
  25 30 35
- cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa  $\phantom{0}$  259 Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln  $\phantom{0}$  45  $\phantom{0}$  50
- gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta 307 Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu 55 60 65
- tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc 355 Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala 70 75 80 85
- aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg 403 Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp 90 95 100
- tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc 451 Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile 105 110 115
- aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca 499 Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala 120 125 130
- tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag 547 Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln

135 140 145 ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct 595 Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro 150 155 ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg 643 Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp 170 175 atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac 691 Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr 185 ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa 739 Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu 200 gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag 787 Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys 215 220 aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc 835 Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe 230 235 gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc 883 Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile 250 931 cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu 265 979 cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr 280 ggc aag gca tot gtt ggc gct cct cca atg tot gtt cct cac ott gac 1027 Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp 295 300 acc cgc gtt atc gag ggt gaa aag ggt ctg ctc ttt gga cct tac ggt 1075 Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu Phe Gly Pro Tyr Gly 315 320 ggc tgg acc cct aag ttc ttg aag gaa ggc tcc tac ctg gac ctg ttc 1123 Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser Tyr Leu Asp Leu Phe 330 aag too ato ogo coa gao aac att oot too tao ott ggo gtt got got 1171 Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr Leu Gly Val Ala Ala cag gaa ttt gat ctg acc aag tac ctt gtc act gaa gtt ctc aag gac 1219 Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr Glu Val Leu Lys Asp 365 cag gac aag cgt atg gat gct ctt cgc gag tac atg cca gag gca caa 1267 Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr Met Pro Glu Ala Gln 380

aac ggc gat tgg gag acc atc gtt gcc gga cag cgt gtt cag gtt attAsn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln Arg Val Gln Val Ile390395	1315
aag oot goa gga tto oot aag tto ggt too otg gaa tto ggo acc acc Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr 410 415 420	1363
ttg atc aac aac tcc gaa ggc acc atc gcc gga ttg ctc ggt gct tcc Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly Leu Leu Gly Ala Ser 425 430 435	1411
cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg 440 445 450	1459
tgc ttc ggt gac cgc atg atc gag tgg ggc gac aag ctg aag gac atg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met 455 460 465	1507
atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu 470 475 480 485	1555
cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala 490 495 500	1600
taaatcttct aactgctttc ttt	1623
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<211> 500 <212> PRT <213> Corynebacterium glutamicum <400> 570 Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp	
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<pre> &lt;211&gt; 500 &lt;212&gt; PRT &lt;213&gt; Corynebacterium glutamicum  &lt;400&gt; 570 Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp 1</pre>	
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435

Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp 130 135 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro 165 170 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala 185 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile 195 205 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys 225 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser 330 Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr 360 Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln 395 Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly 425 Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile

440

Glu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys 490 Leu Glu Glu Ala 500 <210> 571 <211> 1039 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1039) <223> FRXA01615 <400> 571 tatggccaac acttgcattc gggtgctggc gatcatttat gagatgacgc cttgtgttgg 60 tgttcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg 115 Met Ser Asp Ser Pro aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163 Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211 Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu cca age tgg act cag ate gte tte gag egt ttg gat gga eeg gea eaa 259 Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln 40 gag tog toc toc cog tgg aac aat goa gga acc ggc cac tot got ota 307 Glu Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc 355 Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala 70 75 aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg 403 Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp 90 95 tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc 451 Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile aac cet gtt cet cae gta tet tte gge cag gge gea gat cag gtt gea 499 Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala

125

130

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tac a Tyr 1																547
ggc a Gly N 150	-			_	_	_	_	-					_	_		595
ttg a																643
atc q Ile <i>F</i>																691
ctg ( Leu <i>F</i>																739
gtc a Val I	_	-		-	_	-		_	_					_	_	787
aac q Asn V 230	_				_		_			_	_					835
gtc q Val (																883
cca ( Pro (																931
cgt t Arg (																979
ggc a Gly I																1027
acc o Thr A	-	-														1039
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Val V	Val	Leu	Ile 20	Gly	Ala	Gly	Ile	Met 25	Ser	Ser	Thr	Leu	Gly 30	Ala	Met	

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu 35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Pro Trp Asn Asn Ala Gly Thr 50 55 60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly 65 70 75 80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val 85 90 95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$ 

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly 115 120 125

Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp 130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe 145 150 155 160

Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro 165 170 175

Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala 180 185 190

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile 195 200 205

Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp 210 215 220

Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys 225 230 235 240

Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu 245 250 255

Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val 260 265 270

Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His 275 280 285

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                                                                   144
Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
                                                                   192
tee gag eea gea etg ttt gag eag eag tgg gea ege aee eag aag aee
Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
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	gtt att tcc gac Val Ile Ser Asp 75			
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	gac gct ttg gtt Asp Ala Leu Val 125			
	atc aac ttg gag Ile Asn Leu Glu 140			
	cgc ctc atc gag Arg Leu Ile Glu 155			
	ggc acc gct gtg Gly Thr Ala Val 170			
	ctg gat cgc aag Leu Asp Arg Lys			
	gca gcg ggc gtt Ala Ala Gly Val 205			
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gcg gac ctg tt Ala Asp Leu Ph 20	e Ile Gly					Asp		931
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	0		25		30		-	
Pro Leu Arg As	0 p Met Arg	Asp Leu 40	25 Ser Leu	Ala Tyr	Thr Pro	Gly	Val	
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cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac  $\,$  163 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His  $\,$  10  $\,$  15  $\,$  20

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		,,,	_		_	ctg Leu			_					_		1075
					_	ggc Gly	_		-	-	_	-	_	_		1123
						gcc Ala										1171
-			_		_	gcc Ala	_	-	-		_					1219
	_			-		agg Arg 380	_	_			_	_		_	-	1267
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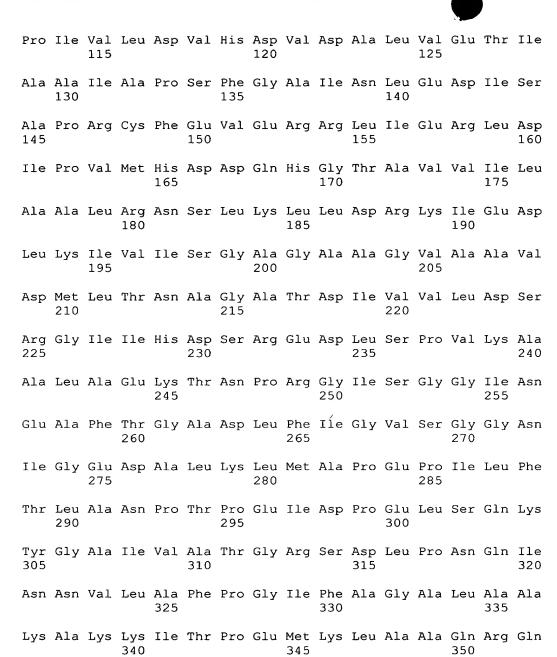
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Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110



Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu

355 360 365

Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg 370 375 380

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Gln 65	Gln	Ser	Arg	Gln	Leu 70	Ser	Arg	Pro	Ser	Pro 75	Lys	Arg	Lys	Thr	Leu 80	
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gcg gac ctg Ala Asp Leu				y Ğly				-	-		931
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His Thr Gly 65	Ile Gly	Asn Thr	Val Ala	a Val	Ile 75	Ser	Asp	Gly	Thr	Ala 80	
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							cca Pro 40									144
							gca Ala									192
							gtc Val									240
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							acc Thr									336
						_	gac Asp 120	_	-	-		_	-	_		384
							gac Asp									432
							gaa Glu									480
		_	-			_	aag Lys	-			_	_	_	_	_	528
act Thr	aca Thr	cct Pro	gct Ala 180	gcg Ala	gca Ala	tcc Ser	gca Ala	act Thr 185	gtg Val	tcc Ser	gct Ala	tct Ser	ggc Gly 190	gac Asp	aac Asn	576
gtt Val																582
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Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala

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Ala	Pro	Ala 35	Glu	Glu	Glu	Glu	Pro 40	Val	Lys	Glu	Glu	Pro 45	Lys	Lys	Glu	
Ala	Ala 50	Pro	Glu	Ala	Pro	Ala 55	Ala	Thr	Gly	Ala	Ala 60	Thr	Asp	Val	Glu	
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Ala	Val 130	Ile	Ala	Arg	Ile	Gly 135	Asp	Ala	Asn	Ala	Ala 140	Ala	Ala	Pro	Ala	
Glu 145	Glu	Glu	Ala	Ala	Pro 150	Ala	Glu	Glu	Glu	Glu 155	Pro	Val	Lys	Glu	Glu 160	
Pro	Lys	Lys	Glu	Glu 165	Pro	Lys	Lys	Glu	Glu 170	Pro	Lys	Lys	Glu	Ala 175	Ala	
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					ctt Leu											211

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gtc ac Val Th		-	_								-	-	-		403
ttc aa Phe As			_	_	_			_			_				451
cac ca His Gl	-			-		_		_		_		_	_		499
gaa go Glu Al		_	_		taaa	atcat	.gg d	ccaaç	gttgt	t tọ	ga				540
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Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn 130 135

115

Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe

120 125

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170 175 180 gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691 Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val 185 190 cgg gga gcc gtc gaa aag cat gag ttt gat gct ggt gtg ttt aac ctt 739 Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala Gly Val Phe Asn Leu 200 205 gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg 787 Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro 215 220 aat atc acg gca atc ggt ttt acc ggt tca cgc cag ggt ggt ttg gca 835 Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg Gln Gly Gly Leu Ala 235 ctg tca cag act gcg ttt agc cgc cca gtt ccc gtt cca gtc ttt gca 883 Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro Val Pro Val Phe Ala 250 931 gaa atg agt gcc acc aac cct gtg ttc gtc ttc ccc ggc gcg ctg gcg Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala 265 gat ttg gat gca tcg agt tcc ttg gct gag gcg ttt acc gct tcc gtc 979 Asp Leu Asp Ala Ser Ser Leu Ala Glu Ala Phe Thr Ala Ser Val 280 acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027 Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075 Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 315 ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123 Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171 Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219 Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267 Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315 Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 395 ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363 Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415

	acg Thr															1411
	ccc Pro															1459
	acg Thr 455															1507
_	gcg Ala					-	_		_	_			_	-		1555
	aga Arg		_	_	_	-						_	-		_	1603
	cca Pro	_		_							_	_			_	1651
	gac Asp	_	taat	agct	gg t	ctti	cacat	it to	jc							1683
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130 135 140 Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala 155 Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu 185 Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala 195 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg 225 230 235 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Leu Ala Glu Ala Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu 375 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val 395 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu 405 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln 425 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile 455

His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val 465 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr 485 490 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp 500 505 Ala Val Pro Arg Glu Ile Asp Arg 515 <210> 589 <211> 1467 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1444) <223> RXN02399 <400> 589 ttgacgcacc aatgcccgat ggagcaatgt gtgaaccacg ccaccacgca aaccgatgca 60 catcacgtcg aaacagtgac agtgcattag ctcatacttt gtg gtc ggc acc gcc 115 Val Val Gly Thr Ala cat tgc gaa tca gca ctt aag gaa gtg act ttg atg tca aac gtt gga 163 His Cys Glu Ser Ala Leu Lys Glu Val Thr Leu Met Ser Asn Val Gly 10 1.5 211 aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro 259 cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp 45 ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 307 Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser 60 355 gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac Glu Ile Leu Trp Asp Ala Val Thr Glu Glu Gly Asp Gly Tyr Ile Asn 70 75 gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 403 Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 451 Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala 105 110 115 aac etc tee gge cac ace tae eet gae cag tee etc tae eea geg aac 499 Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn

	120				125					130				
tcc gtt Ser Val 135			-	_	_				_	_	_	-		547
gat gaa Asp Glu 150	_	_		-		-			_	_			-	595
gtc cca Val Pro	_		_		_	_					_			643
gtc tac Val Tyr	Glu Le	_	_	_	_		_	_		_	-			691
cac tgg His Trp		_		-		-	_	_	-					739
ggc aag Gly Lys 215	_	_				_			_		_			787
gcc cgc Ala Arg 230	_	-	-	_	-					-	_		_	835
cgt acc Arg Thr	-		-	_		_				_	_	_		883
cgc gac Arg Asp	Gln P						_		_	_				931
cac gtc His Val	_					-		-	_	-	-			979
gca cca Ala Pro 295														1027
gag ctc Glu Leu 310	-	_		_	_		-	_					-	1075
cag ctg Gln Leu	_			_								_		1123
ctc gag Leu Glu	Ala As													1171
ggc ttc Gly Phe	_	_					_							1219

tac ggc atg tto Tyr Gly Met Pho 375		Tyr Gly Tyr			
tcc ttc gtt gad Ser Phe Val Asp 390					
ggc ttc acc gct Gly Phe Thr Ala					,
gac cag atc gca Asp Gln Ile Ala 425	a Thr Thr Val	-		3	
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aat				1467	
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Trp Asp Thr Asi	n Pro Arg Trp	Asn Gly Ile 40	Thr Arg Asp	Tyr Thr Ala	
Asp Gln Val Ala	a Asp Leu Glr 55	_	Ile Glu Glu 60	His Thr Leu	
Ala Arg Arg Gly	y Ser Glu Ile 70	e Leu Trp Asp	Ala Val Thr 75	Gln Glu Gly 80	
Asp Gly Tyr Ile	e Asn Ala Lei 85	ı Gly Ala Leu 90	Thr Gly Asn	Gln Ala Val 95	
Gln Gln Val Ard	-	Lys Ala Val 105	Tyr Leu Ser	Gly Trp Gln 110	
Val Ala Gly Asp 115	o Ala Asn Leu	Ser Gly His 120	Thr Tyr Pro 125	Asp Gln Ser	
Leu Tyr Pro Ala	a Asn Ser Val		Val Arg Arg 140	Ile Asn Asn	
Ala Leu Leu Ard 145	g Ser Asp Gli 150	ı Ile Ala Arg	Thr Glu Gly 155	Asp Thr Ser 160	
Val Asp Asn Tr	o Val Val Pro	lle Val Ala	Asp Gly Glu	Ala Gly Phe	

				165					170					175	
Gly	Gly	Ala	Leu 180	Asn	Val	Tyr	Glu	Leu 185	Gln	Lys	Ala	Met	Ile 190	Ala	Ala
Gly	Ala	Ala 195	Gly	Thr	His	Trp	Glu 200	Asp	Gln	Leu	Ala	Ser 205	Glu	Lys	Lys
Cys	Gly 210	His	Leu	Gly	Gly	Lys 215	Val	Leu	Ile	Pro	Thr 220	Gln	Gln	His	Ile
Arg 225	Thr	Leu	Asn	Ser	Ala 230	Arg	Leu	Ala	Ala	Asp 235	Val	Ala	Asn	Thr	Pro 240
Thr	Val	Val	Ile	Ala 245	Arg	Thr	Asp	Ala	Glu 250	Ala	Ala	Thr	Leu	Ile 255	Thr
Ser	Asp	Val	Asp 260	Glu	Arg	Asp	Gln	Pro 265	Phe	Ile	Thr	Gly	Glu 270	Arg	Thr
Ala	Glu	Gly 275	Tyr	Tyr	His	Val	Lys 280	Asn	Gly	Leu	Glu	Pro 285	Cys	Ile	Ala
Arg	Ala 290	Lys	Ser	Tyr	Ala	Pro 295	Tyr	Ala	Asp	Met	Ile 300	Trp	Met	Glu	Thr
Gly 305	Thr	Pro	Asp	Leu	Glu 310	Leu	Ala	Lys	Lys	Phe 315	Ala	Glu	Gly	Val	Arg 320
Ser	Glu	Phe	Pro	Asp 325	Gln	Leu	Leu	Ser	Tyr 330	Asn	Cys	Ser	Pro	Ser 335	Phe
Asn	Trp	Ser	Ala 340	His	Leu	Glu	Ala	Asp 345	Glu	Ile	Ala	Lys	Phe 350	Gln	Lys
Glu	Leu	Gly 355	Ala	Met	Gly	Phe	Lys 360	Phe	Gln	Phe	Ile	Thr 365	Leu	Ala	Gly
Phe	His 370	Ser	Leu	Asn	Tyr	Gly 375	Met	Phe	Asp	Leu	Ala 380	Tyr	Gly	Tyr	Ala
Arg 385	Glu	Gly	Met	Thr	Ser 390	Phe	Val	Asp	Leu	Gln 395	Asn	Arg	Glu	Phe	Lys 400
Ala	Ala	Glu	Glu	Arg 405	Gly	Phe	Thr	Ala	Val 410	Lys	His	Gln	Arg	Glu 415	Val
Gly	Ala	Gly	Tyr 420	Phe	Asp	Gln	Ile	Ala 425	Thr	Thr	Val	Asp	Pro 430	Asn	Ser
Ser	Thr	Thr 435	Ala	Leu	Lys	Gly	Ser 440	Thr	Glu	Glu	Gly	Gln 445	Phe	His	Asn

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<sup>&</sup>lt;212> DNA <213> Corynebacterium glutamicum

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	aag Lys															739
	cgc Arg 215															787
_	acc Thr	_	_		-	_		_				_	_	_		835
	gac Asp										_	_				883
	gtc Val	_						_		-	_	_	_			931
-	cca Pro		_	_	_			-						_	_	979
	ctc Leu 295															1027
_	ctg Leu	_				-								_		1075
	gag Glu															1123
	ttc Phe			_					_							1171
	ggc Gly															1219
	ttc Phe 375															1267
	ttc Phe					His										1315
-	cag Gln		_			_	_	_						_	-	1363
	ggt Gly										tago	gacct	ac a	iggtt	ctgac	1416
aat																1419

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<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 592

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Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala 20 25 30

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu 35 40 45

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
50 55 60

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val 65 70 75 80

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln 85 90 95

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser 100 105 110

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn 115 120 125

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser 130 135 140

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe 145 150 155 160

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala 165 170 175

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys 180 185 190

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile 195 200 205

Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro 210 215 220

Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr 225 230 235 240

Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr 245 250 255

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala 260 265 270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr 275 280 285 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg 295 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys 325 330 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly 345 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala 355 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys 375 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val 385 390 Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn

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					gcc Ala											307
					cgc Arg 75											355
					ggc Gly											403
		_			tac Tyr	_	_				_	_	_	_		451
					gat Asp											499
		_			ctg Leu		_	_			_		-	-		547
_	_				ctc Leu 155				_					_		595
	_		_		gct Ala	_	_		_				_	-	_	643
					gag Glu											691
	_	_		_	tcg Ser		_	_	_		_					739
_		_		_	gcc Ala				_	_	_		_	_		787
	-	-			cgt Arg 235								_		_	835
					acc Thr											883
					ggc Gly											931
					atc Ile											979
gca	gct	gtt	gat	gct	gaa	gac	aag	acc	tta	ggt	tac	tct	aac	tgg	ttc	1027

Ala	Ala 295	Val	Asp	Ala	Glu	Asp 300	Lys	Thr	Leu	Gly	Tyr 305	Ser	Asn	Trp	Phe	
	ctc Leu				_	_		_		_		-			_	1075
	ttc Phe			-			-	-	-	-				_		1123
	acc Thr															1171
-	ggt Gly			_						-		_			-	1219
	ttc Phe 375	_			_	_	_	_	_			_	_	_		1267
	gga Gly		_	-	_		_	_	_							1315
	tac Tyr			_		-	_				_	-	_			1363
	aac Asn					_	_		_	_		_	_		-	1411
	acc Thr	_	_	_		_	_	-			-	_	_			1459
	ctg Leu 455	_	_	-		-	_	_	_	_	_	_	_			1507
	act Thr															1555
	gca Ala															1603
	cag Gln															1651
	cct Pro		_	_	_			_		_			-		-	1699
	atg Met															1747

gcc acc acc acc ttg gtt gst gst gcg acg acg acg acg acg acg acg acg acg	535		540	5	545										
Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg 580	Ala Asn Thr	Ala Trp Val		Thr Gly A		His Ala									
Ala Ála Ála Ály Arg Arg Arg Ásp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr 595  gca cca aac aac tagt tcg tct gag gaa gaag aag aag aag gag atg gac acg acc alc acc act act ctc gga tac glt gtg cgc tgg gtt gag cac leac Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His 625  ggt gtt ggt tgc tcc aag gtt cca gac act cat gac atc gac ctc atg Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met 630  gaa gac cgc gca acg ctc gtt gtt cca gac atc cat gac atc gac ctc atg Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met 630  gaa gac cgc gca acg ctc gtt att tcc tcg cag atg ctg gcc act tcg Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Ash Trp 6650  atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu 675  cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac act gac atg gcd atg gad atg lea Gry 685  cgc atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gac ctac 2179  Arg Met Ala Val Val Val Asp Lys Gln Ash Ala Gly Asp Glu Ala Tyr 680  aag gac ttg att ttc gaa gac acc aag tcc ccc tcc gcc ttc cag gcg gct 227  Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala 695  aag gac ttg att ttc gaa ggc acc aag tcc ccc tcc gcc ttc cag gcg gcc tcc 227  Arg Asp Met Ala Pro Lys Tyr Asp Arg Arg Glu Phe Lys Ash 730  aag gac ttg att ttc gaa gcc ccc aag tcc aaa gcc aaa aac aac acc acc gcg ccc acc a	_	His Leu Val		Lys Val G		Leu Arg									
Ala Pro Asn Thr Asn Trp Ser Glu Glu Lys Lys Glu Glu Met Asp 600 605 605 605 610 Lys Lys Glu Glu Met Asp 610 600 605 605 610 Lys Lys Glu Glu Met Asp 610 600 605 605 610 Lys Lys Glu Glu Met Asp 615 620 625 625 625 625 625 625 625 625 625 625		Arg Arg Asp	Ser Leu Arg	Asn Ile L	eu Thr Ile										
Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His 615    ggt gtt ggt tgc tcc aag gtt cca gac atc gac atc gac ctc atg 620    ggt gtt ggt tgc tcc aag gtt cca gac atc gac atc gac ctc atg 630    gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg    Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp    650    atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa    11e Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu    670    685    cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac    Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr    680    cgc gat atg gcc cg aag tac gac gcc tcc ctc gcc ttc cag gcg gct    Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala    695    aag gac ttg att tc gaa ggc acc aag tcc cat gg gc tac acc gag    2227    Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala    695    aag gac ttg att tc gaa ggc acc aag tcc cat gg gc tac acc gag    2227    Arg Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu    710    715    ccc atc ttg cac gca cgc cgc ggc gag ttc aaa    2317    taagcacgct tttcgacgct tac    2340	Ala Pro Asr	Thr Asn Trp	Ser Glu Glu		ys Glu Glu										
Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met 645  gaa gac cgc gca acg cgt cgt cgt att tcc tcg cag atg ctg gcc aac tgg 2083 Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp 655  atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa 111e Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu 675  cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac 670  cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac 680  cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac 680  cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala 705  aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu 710  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aaac gca aaa aac C2179  ccc atc ttg cac gca cgc cgc cgc gag ttc aacc gag cac aac acc gag cac aacc gcc cgc cg	Asn Asn Cys		Leu Gly Tyr	Val Val A	rg Trp Val										
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp 650    atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa   Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu 675    cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr 680    cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Ala 695    aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu 715    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2275    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc Ala Lys Asn 730    cac atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc Ala Lys Asn 730    cac atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2317    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa acc   2340    c210> 594    Met Thr Glu Gln Glu Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly	Gly Val Gly	Cys Ser Lys		Ile His A		Leu Met									
The Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu 665    cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac 2179   Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr 680    cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct 2227   Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala 695    aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag 2275   Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu 715    ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac 2317   Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys Ala Lys Asn 730    taagcacgct tttcgacgct tac 2340		, Ala Thr Leu	-	Ser Gln Me	et Leu Ala	Asn Trp									
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50 55 60

Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met 65 70 75 80

Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu 85 90 95

Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro
100 105 110

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Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala 130 135 140

Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr 145 150 155 160

Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu 165 170 175

Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe 180 185 190

Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu
195 200 205

Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser 210 215 220

Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn 225 230 235 240

Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile 245 250 255

Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr 260 265 270

Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp 275 280 285

Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly 290 295 300

Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met 305 310 315 320

Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val

Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu 340 345 350

Leu Phe Val Arg Asn Val Gly His Leu Met Gln Asn Pro Ser Ile Leu 355 360 365

Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met Asp Ala Val Leu Thr 370 375 380

Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn 385 390 395 400

Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro 405 410 415

Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly Arg Val Glu Asp Leu
420 425 430

Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly Val Met Asp Glu Glu 435 440 445

Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile Met Glu Val Ala Asp 450 460

Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu 465 470 475 480

Ile His Thr Ser Met Glu Ala Gly Ala Met Val Arg Lys Ala Asp Met 485 490 495

Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn Asn Asn Val Asp Ala 500 505 510

Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln Ile Gly Lys Gly Met 515 520 525

Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu Glu Lys Lys Ile Gly 530 540

Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly 545 550 555 560

Ala Thr Leu His Ala Thr His Tyr His Leu Val Asp Val Phe Lys Val
565 570 575

Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile 580 585 590

Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys
595 600 605

Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val 610 615 620

Arg Trp Val Glu His Gly Val Gly Cys Ser Lys Val Pro Asp Ile His 625 630 635 640

Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln 645 650 655

Met Leu Ala Asn Trp Ile Arg His Asp Val Val Ser Lys Glu Gln Val

660 665 670 Leu Glu Ser Leu Glu Arg Met Ala Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu 690 695 Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro 715 Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys 730 Ala Lys Asn <210> 595 <211> 2159 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(2136) <223> FRXA02404 <400> 595 atg cag gtt gca aaa gtt ctc tac gac ttt gta acc gaa gcg gta ctc 48 Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu cct cgc gtg ggt gtg gat gcg gaa aag ttc tgg tcc gga ttc gcc gcc 96 Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala ate gee egg gae ete ace eea ege aac ege gag etg ett get ege ege 144 Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg 192 gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac 240 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr 70 ttg gtt gag gag cca gaa gct gca gaa atc cgt acc caa aac gtc gat 288 Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp acg gaa atc tcc agc acc gca gga cct cag ctg gtt gtt cca att ctg 336 Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu 100 105 aac gca cgc ttc gcg ctg aac gct gcc aat gct cgc tgg ggt tcc ctc 384 Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu 115 120

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						aac Asn										480
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						ctt Leu 215	_		_	_		_	_	_		672
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_		_		_		aag Lys 295			_				_			912
						att Ile										960
						ttc Phe										1008
						gat Asp										1056
						gtt Val										1104
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Asn	Lys 370	Met	Arg	Asn	Ser	Arg 375	Lys	Gly	Ser	Ile	Tyr 380	Ile	Val	Lys	Pro	
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_	_	-		-	ctt Leu	_	_		_			_	_	-		1248
					cgt Arg											1296
_	-	_	_	_	cgc Arg	_	_							_	_	1344
_			_	_	atc Ile				_	_	_		-	_		1392
	_	_	_	_	cag Gln 470		_	_		_	_	_				1440
		_	-	_	ggt Gly											1488
					tgg Trp											1536
					cag Gln											1584
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					caa Gln 550											1680
_	_	_			ctc Leu					_						1728
		_	_	_	aag Lys	_	-	_	_			_	-			1776
					cgc Arg											1824
					gac Asp											1872

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His	Ala	Asp	Val 180	Glu	Lys	Tyr	Asn	Ile 185	Thr	Asp	Gly	Lys	Leu 190	Ala	Ala
His	Ile	Gly 195	Asp	Ser	Val	Tyr	Arg 200	Leu	Lys	Asn	Arg	Glu 205	Ser	Tyr	Arg
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Lys	Ala	Asp	Lys	Thr 245	Gly	Leu	Lys	Asp	Ile 250	Val	Leu	Glu	Ser	Ala 255	Ile
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Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val 515 520 525

Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val 530 535 540

Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp 545 550 560

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Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile 580 585 590

Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys 595 600 605

Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu 610 615 620

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					gct Ala										211
_		_	-		gag Glu			_	_	_	_		_		259
					aat Asn 60										307
 _	_	_			gaa Glu	_							_	-	355
_		-			ttg Leu	_		-	-	_		_	_	-	403
		_	_		tca Ser	_		_		_					451
_		_		_	caa Gln		-	_		_	_	-	-	-	499
					tat Tyr 140										547
	_				ctt Leu		-	_		-					595
			_		ttc Phe			_	_						643
					gtt Val										691
					gat Asp			-					-	-	739
					caa Gln 220										787
			-		cac His		-		-			-		_	835

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Leu Gly Tyr Asp Gly Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu

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230

Thr Thr Ala Gly Leu Gly Trp Leu Glu Leu 245 250

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Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp
tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc
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Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser
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                                                                   307
Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg
gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag
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Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys
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ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag
                                                                   403
Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln
gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc
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Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu
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Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala
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Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro
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                                                                   595
Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala
gtc aat cac ccg aat ctg cgc ctc aac ctg gat ttg tac cac gcc cag
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Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln
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				gtc Val												835
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Gly	Leu	Gly	Pro 100	Gln	Gly	Leu	Pro	Val 105	Thr	Pro	Ile	Glu	Val 110	Val	Thr	
Pro	Glu	Met 115	Trp	Leu	Tyr	Ala	Ala 120	Glu	Thr	Leu	Arg	Gln 125	Ile	Ala	Glu	
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Ala 145	Val	Asp	His	Pro	Gly 150	Thr	Pro	Phe	Ala	Lys 155	Ala	Thr	Asp	Thr	Leu 160	
Ala	Leu	Val	Lys	Ala	Val	Asn	His	Pro	Asn	Leu	Arg	Leu	Asn	Leu	Asp	

165 175 170 Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg 185 Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp 225 230 Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val <210> 601 <211> 1575 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (41)..(1552) <223> RXN03117 <400> 601 tgtgcaacat tagttcgtta agaagagtca cattccagcc atg att acc cac gaa 55 Met Ile Thr His Glu gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg 103 Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu 10 get cae aag atg get ege gtt gea gee gae eea gtt gag gtt get geg 151 Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg 199 Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val 40 cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg 247 Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt 295 Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly 75 ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act 343 Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr 95 gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac 391

Ala	Val	Arg	Glu 105	Leu	Asp	Phe	His	Asp 110	Thr	Phe	Leu	Ala	Ala 115	Glu	Tyr	
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					aag Lys											487
					ttg Leu 155											535
					cat His											583
					gat Asp											631
_	_				acg Thr		_									679
					ttt Phe											727
					gca Ala 235											775
					ggc Gly	-				_	_				_	823
					cct Pro	_		_	-		_	_		-	_	871
					acc Thr											919
					gcg Ala											967
					gat Asp 315		_			-	_					1015
					atc Ile								Gln			1063
_		-	_	_	cga Arg	-			-				_			1111

345		350	355
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gat gga acc gtc g Asp Gly Thr Val V 425			
ctg gga gca cgg c Leu Gly Ala Arg E 440			
acc ttg gct gaa g Thr Leu Ala Glu G 455			
gat gcg gca cag c Asp Ala Ala Gln A 470			
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Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly 65 70 75 80

Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala 85 90 95

Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe 100 105 110

Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu 115 120 125

Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly 130 135 140

Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys 145 150 155 160

Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro Ser Ala 165 170 175

Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr 180 185 190

Gln Ala Ile Gly Gln Ala Leu His Thr Thr Ala Thr Arg Gln Ser 195 200 205

Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala 210 215 220

Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly 225 230 235 240

Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu 245 250 255

Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly 260 265 270

Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala 275 280 285

Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu 290 295 300

Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val 305 310 315 320

Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly Ser Asn 325 330 335

Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His 340 345 350

Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His 355 360 365

His Glu Arg Ser Tyr Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile 370 375 380

Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg

385 390 395 400 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala 410 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val 425 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu 455 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu Gly Leu Phe 500 <210> 603 <211> 975 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(975) <223> FRXA00406 <400> 603 gac cca gtt gag gtt gct gcg gac act cag gaa atg atc atc acc cgc 48 Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca 96 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro gtt age tet gee egt geg atg gea eag gte agg eea gtt ace gat ggt 144 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly 35 40 egg ggt gea tet gtt tte ggt etg eea gga egt tat gee geg gaa tgg 192 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp 50 55 gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac 240 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp 65 acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg 288 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro 85 90 att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc 336 Ile Leu Ala Ala Gln Gln Ala Gly Lys Gly Lys Asp Leu Ile

			100					105					110		
_			_		Gly				_	_		_		_	 384
_	_	_			cac His	_		_		_	-				432
					atc Ile 150								_	_	480
		_	_		ggt Gly	_	-	_				_		_	 528
					gcg Ala										576
			_	_	tcc Ser			_	_	_	_	_	_	_	 624
		_	_		cca Pro			-		-	-		_		 672
					ctt Leu 230										720
_		_	_		cga Arg	_		_	_				_	_	768
					tca Ser										816
					gca Ala										864
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	cac His														975

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Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp 50 55 60

Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp 65 70 75 80

Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro 85 90 95

Ile Leu Ala Ala Gln Gln Ala Gly Lys Gly Lys Asp Leu Ile 100 105 110

Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
115 120 125

Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro 130 135 140

Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr 145 150 155 160

Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg 165 170 175

Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala 180 185 190

Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly 195 200 205

Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala 210 215 220

Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala 225 230 235 240

Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His 245 250 255

Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met 260 265 270

Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser 275 280 285

Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly 290 295 300

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Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu 305 310 315 320

Asp His Ser Ile Met

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cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala 35 40 45

gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val 50 55 60

gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac 240
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
65 70 75 80

att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa 288 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
85 90 95

cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat 336 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp 100 105 110

ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct 384 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala 115 120 125

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tac etc etg tgg cac ggc gag etg ecc act geg caa caa ett geg gag

Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu

60

307

ttc a Phe A 70																355
tcc o	_				-			_	_		_	_	_	_	_	403
cgc a																451
acc o																499
ctt c Leu F	_	_			-	_	_		-	-	-	-			_	547
atc a Ile 1 150		_		_		_	_		-	_	_		_	-		595
atg ( Met \						_	_			_				_	-	643
gtc o																691
aac q Asn A	_					_	_									718
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Phe C	Glu 50	Glu	Val	Phe	Туr	Leu 55	Leu	Trp	His	Gly	Glu 60	Leu	Pro	Thr	Ala	
Gln 6	Gln	Leu	Ala	Glu	Phe 70	Asn	Glu	Arg	Gly	Arg 75	Ser	Tyr	Arg	Ser	Leu 80	

Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His

85 90 95

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Glu	Asn	Leu	Leu	Ser 165	Met	Val	Phe	Gly	Thr 170	Gly	Pro	Glu	Ser	Pro 175	Ala	
Ser	Asn	Pro	Ala 180	Asp	Val	Arg	Asp	Phe 185	Glu	Lys	Ser	Leu	Ile 190	Leu	Tyr	
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				ttc Phe											ttc Phe	144
_	-	_		ttc Phe		_	_		-							192
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Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
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                                             Met Thr Glu Ser Gln
gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc
                                                                   163
Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro
gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt
                                                                   211
Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val
gec att ggc gca etg gat gec gaa eeg att gte gee att ega gga ete
                                                                   259
Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu
                             45
ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggc
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Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly
                         60
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							tac Tyr									403
	_	_				-	gtg Val		-	-	_	_	_	_		451
_				_	_		acc Thr 125	_		_		_		-	-	499
							gca Ala									547
							gca Ala									595
							atc Ile									643
	-		_	_		_	gtc Val		_				_	_		691
							cac His 205									739
							att Ile									787
		-					tcc Ser	_			_				_	835
		_	_	_	_	-	agc Ser	_	_	_				_		883
							cag Gln									931
							aat Asn 285									979
							tac Tyr									1027

ggc gac aaa ca Gly Asp Lys Gl 310		_	_		-		_	1075
ccg tgg atg ct Pro Trp Met Le								1123
cag tac gaa cc Gln Tyr Glu Pr 34	Ser Arg	-	-			_	_	1171
aag aaa atc ga Lys Lys Ile Gl 360		_	-		-			1219
gac cac atg cc Asp His Met Pr 375	-	_	-			_	, ,	1267
ttc aaa gct tc Phe Lys Ala Se 390	_	_			-			1315
gat tgg gac aa Asp Trp Asp As								1363
acc ggt gaa ga Thr Gly Glu Gl 42	ı Leu Arg	_	_	-		-		1411
gat agc cga ca Asp Ser Arg Gl 440		-	_		-	_		1459
acc acc cgc ag Thr Thr Arg Se 455		tt tgaaa	aggagc to	ca				1494
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Asn Asp Ala Se		Ala Val	Glu Gln 25	Leu Lys	Ile Arg 30	Val	Leu	
Asp Thr Val Gl	y Val Ala	Ile Gly 40	Ala Leu	Asp Ala	Glu Pro 45	Ile	Val	
Ala Ile Arg Gl 50	y Leu Leu	Glu Asp 55	Leu Gly	Gly Thr 60	Glu Gln	Ser	Thr	
Leu Ile Gly Gl 65	y Gly Lys 70	Thr Ser	Pro Glu	Arg Ala 75	Ala Phe	Phe	Asn 80	

385

390

395

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys 85 Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala 105 Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala 120 Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg 135 Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys His Asn Ala Glu Ile His Ser Gln Ser Ala Leu 265 Asp Ala Ala Gln Glu Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile 295 Gly Gly Glu Glu Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu 315 Ala Asp His Ser Leu Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp 345 Val Gln Thr Leu Met Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe 355 Ser Asp Arg Phe Pro Asp His Met Pro Ala Asp Leu Glu Val Thr Leu 375 380 Asn Asp Gly Ser Val Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe

His Asp Asn Pro Leu Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala 405 410 415

Leu Val Thr Pro Phe Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr
420 425 430

Ile Ile His Glu Leu Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala 435 440 445

Leu Ala Lys Val Ser Thr Thr Arg Ser 450 455

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<223> RXN03144

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gat cgt gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc 144
Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
35 40 45

gaa gac ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat 192 Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr 50 55 60.

cat gtg cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag 240 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu

act tac aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att 288
Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
85 90 95

gat ctg gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg 336 Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr

gaa cac att gca gag att gtg ctg cgc acc agt cac cac acg cat tat 384 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr 115 120 125

gtg att ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc 432 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala 130 135 140

tcg cgt gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg 480

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Ser 145	Arg	Glu	Thr	Leu	Asp 150	His	Ser	Ile	Met	Tyr 155	Ile	Phe	Ala	Val	Ala 160	
					tgg Trp								-	_	_	528
		_	_	_	act Thr			_			-		_			576
	_		_		acg Thr	-	_				_	_		_		624
					aaa Lys											672
		_	-	_	gct Ala 230	-		_	-		_	_		_		720
_					aat Asn			-			_				_	768
					tca Ser											816
_	_		-	-	gat Asp	_		-	_				-	-	_	864
	_		_	-	gcg Ala	-				_		tgaa	atcto	ctt		910
ttc	gaato	ggt o	gtt													923
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	0> 61 Thr		Ala	Thr 5	Arg	Gln	Ser	Arg	Lys 10	Gly	Glu	Ile	Ser	Ser 15	Trp	
Lys	Ala	Phe	Ala 20	Pro	Ala	Phe	Ala	Gly 25	Lys	Met	Ala	Ile	Glu 30	Ala	Met	
Asp	Arg	Ala 35	Met	Arg	Gly	Glu	Gly 40	Ser	Pro	Ala	Pro	Ile 45	Trp	Glu	Gly	
Glu	Asp 50	Gly	Val	Ile	Ala	Trp 55	Leu	Leu	Ser	Gly	Lys 60	Asp	His	Val	Tyr	
		-	_	_					_	_	_			_		

His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu

65 70 75 80 Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr 105 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr 120 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala 130 135 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala 150 Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg 165 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys 200 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg 225 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln 245 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu 295 <210> 615 <211> 511 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(511) <223> FRXA02322 <400> 615 cgcgcagagc taaactgcgt gaggttgtgg cctgtcacac ataatcggcc tagggtggga 60 ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115 Met Arg Ile His Asp

gtt tat acc Val Tyr Thr							
gcg tgg aaa Ala Trp Lys						Thr Pr	
gat gtt tcg Asp Val Ser 40			Arg Ile	_			_
tct gcc gcg Ser Ala Ala 55							
gcg cag tcc Ala Gln Ser 70	His Pro A			_		Ile Se	
ggc agc tac Gly Ser Tyr							
cgt gaa ttg Arg Glu Leu						Ser Hi	
ccc ggc gac Pro Gly Asp 120			Leu Ala				
agc agc ggc Ser Ser Gly 135							511
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Lys Ala Glu	His Leu A	la Trp Lys	Phe Ser 25	Glu Leu	Ala Thr	-	0
Val Glu Val 35	Thr Pro A	sp Val Ser 40		Ile Ile	Asn Arg 45	Ile Il	е
Asp Asn Ala 50	Ala Val S	er Ala Ala 55	Ser Val	Leu Arg 60	Arg Pro	Val Th	r
Val Ala Arg 65		la Gln Ser 70	His Pro	Arg Glu 75	Lys Gly		s 0

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala 85 90 95

Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala 100 105 110 110 Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val

115 120 125

Ala Gln Ala Gln Arg Ser Ser Gly Arg 130 135

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<223> RXA02329

<400> 617

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ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt 96
Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
20 25 30

gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac 144
Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
35 40 45

ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat cat gtg 192 Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val 50 55 60

cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac  $\phantom{0}$  240 Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr  $\phantom{0}$  65  $\phantom{0}$  70  $\phantom{0}$  75  $\phantom{0}$  80

aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att gat ctg 288
Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
85 90 95

gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac 336 Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His 100 105 110

att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile

115 120 125

ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tcg cgt 432 Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg 130 135 140

gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa 480 Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln 145 150 155 160 gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr

165 170 175

cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp

180 185 190

cct gaa tgg acg cgc cga tac cat tct

Pro Glu Trp Thr Arg Arg Tyr His Ser

195 200

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<213> Corynebacterium glutamicum

<400> 618

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Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg 20 25 30

Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp 35 40 45

Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
50 55 60

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr 65 70 75 80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu 85 90 95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
100 105 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile 115 120 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg 130 135 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln 145 150 155 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr 165 170 175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp 180 185 190

Pro Glu Trp Thr Arg Arg Tyr His Ser 195 200

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                                            Met Ser Asp Ser Gln
gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc
                                                                   163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg
                                                                   211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg
                                                                   259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
         40
                             45
tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg
                                                                   307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc
                                                                   355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
cac tee tta eec aac ace tge cac eec atg gae gtg etg ege ace gea
                                                                   403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
gtg tee tae atg ggt ace ttt gat eee gat eeg ttt ace ege gat gee
                                                                   451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
            105
                                110
gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg
                                                                   499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
        120
                            125
gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca
                                                                   547
Val Val Ala Met Asp Ile Arg Arg Ser Gly Glu Glu Ile Ile Ala
cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt
                                                                   595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
                    155
                                        160
ggc aat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat
                                                                   643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
                170
                                    175
ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc
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Phe	Glu	Arg	Ser 185	Leu	Ile	Leu	Tyr	Ala 190	Glu	His	Ser	Phe	Asn 195	Ala	Ser	
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									aaa Lys							787
				_	_			_	ctg Leu	_		_	-			835
	_	_	_		_		_		ttg Leu 255	_	_		-	_		883
					-				aac Asn		_			_		931
	_				_	_			gct Ala	_	_		_			979
									caa Gln							1027
									ccg Pro							1075
_	_				_	-			aca Thr 335		-			_	_	1123
				Trp					gtg Val							1171
gcg Ala	ctg Leu	atc Ile 360	cga Arg	cca Pro	ttg Leu	tct Ser	gcc Ala 365	tac Tyr	aac Asn	gga Gly	gtg Val	gaa Glu 370	gaa Glu	agg Arg	gag Glu	1219
					gag Glu			taat	cagt	ga g	gcto	gattt	c ta	ıa		1266
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	)> 62 Ser		Ser	Gln	Val	Λκα	Tue	Clv	Ī.au	Asn	Clv	Val	Tlo	Sor	Aen	

Met Ser Asp Ser Gln Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp 1 5 10 15

Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr 20 25 30

Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu 35 40 45

Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu 50 55 60

Arg Thr Phe Asn Thr Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly 65 70 75 80

Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp 85 90 95

Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro 100 105 110

Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu 115 120 125

Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Ser Gly 130 135 140

Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe 145 150 155 160

Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala 165 170 175

Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His 180 185 190

Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg 195 200 205

Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly 210 215 220

Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp 225 230 235 240

Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp 245 250 255

Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly 260 265 270

Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala 275 280 285

Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu 290 295 300

Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala 305 310 315 320

Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro 325 330 335

Leu Phe Val Leu Ala Arg Val Ser Gly Trp Thr Ala His Ile Val Glu

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gtc tcg gcc cgg Val Ser Ala Arg 150					595
gcc gct gga gtg Ala Ala Gly Val					643
tac tta gat gcg Tyr Leu Asp Ala 185	Gly Ala Asp	_		_	691
gaa gcc gac ttc Glu Ala Asp Phe 200	-		•		739
ctg gcg aat atg Leu Ala Asn Met 215	_	e Gly Lys Thr			787
gtg ttg gaa gag Val Leu Glu Glu 230					835
ctg cgt att gcc Leu Arg Ile Ala			-	-	883
gaa cac ggt acc Glu His Gly Thr 265					931
aga tta tat gag Arg Leu Tyr Glu 280			_		979
cac att ttc acc His Ile Phe Thr 295		Gly Glu Asn		cagccaa	1025
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Phe Ser Pro Leu 35	Ile Ala Arç	Ser Ile Glu 40	Glu Ala Gly 45	Phe Glu Gly	

Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp 50 55 60

Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile
65 70 75 80

Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe 85 90 95

Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala 100 105 110

Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys 115 120 125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg 130 135 140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile 145 150 155 160

Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile 165 170 175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr  $180 \,$   $185 \,$  190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile 195 200 205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr 210 215 220

Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile 225 230 235 240

Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala 245 250 255

Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg 260 265 270

Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr 275 280 285

Asn Val Phe Asp Gln His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn 290 295 300

Glu 305

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<223> FRXA02333

<400> 623

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		_	_		gaa Glu	-			_		-					192
	cc tac aga aaa gga gaa aac aat gag tgacagccaa gtccgcaaag Thr Tyr Arg Lys Gly Glu Asn Asn Glu 65 70															239
gac																242
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Ala	Met	Gly	Gln 20	Val	Glu	Gln	Ala	Leu 25	Ala	Glu	Ile	Lys	Glu 30	His	Gly	
Thr	Gln	Glu 35	Gly	Trp	Leu	Asp	Arg 40	Met	Gln	His	Arg	Ser 45	Arg	Leu	Tyr	
Glu	Leu 50	Leu	Arg	Tyr	Glu	Asp 55	Tyr	Asn	Val	Phe	Asp 60	Gln	His	Ile	Phe	
Thr 65	Tyr	Arg	Lys	Gly	Glu 70	Asn	Asn	Glu								
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	aag Lys													-		211
	tgg Trp															259
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Tyr	Val	Asp	Asp	Val 85	Gln	Glu	Glu	Tyr	Asp 90	Ser	Leu	Lys	Asp	Lys 95	Gly	
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                                             Met Thr Ser Ile Pro
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Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
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His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg
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Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
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Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
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Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
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Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
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His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
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Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
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						_	aag Lys 605	_		_				_	_	1939
	-	_	_	_			gcc Ala		_	_	_		_	_		1987
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cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp 680 685 690	2179
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Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys 490 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr 505 Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly 530 535 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly 565 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala His Leu Gly Phe Asp Leu Asp Val Asp Val Asn 725 730

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					aaa Lys											931
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Glu Ala Gln Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
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Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp 65 70 75 80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala 85 90 95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala 100 105 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val 115 120 125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp 130 135 140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser 145 150 155 160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val 165 170 175

Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile 180 185 190

Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr 195 200 205

Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr 210 215 220

Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His 225 230 235 240

Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu 245 250 255

Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp 260 265 270

Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met 275 280 285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp 290 295 300

Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser 305 310 315 320

Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp 325 330 335

Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr 340 345 350

Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu 355 360 365

Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu 370 380

Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala 385 390 395 400

Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala 405 410 415

Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala 420 425 430

Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg 435 440 445

Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn 450 455 460

Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp 465 470 475 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys 485 490 495

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Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn 515 520 525

Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly 530 535 540

Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu 545 550 555 560

Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly 565 570 575

Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu 580 585 590

Ala Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln 595 600 605

Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp 610 615 620

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						cag Gln										691
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<400> 632

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Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
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Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe 65 70 75 80

Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr 85 90 95

Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu 100 105 110

Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu 115 120 125

Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu 130 135 140

Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val 145 150 155 160

Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala 165 170 175

Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser 180 185 190

His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser 195 200 205

Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser 210 215 220

Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala 225 230 235 240

Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu 245 250 255

Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
260 265 270

Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg 275 280 285

Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His

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295

300

290

COCHTAN OS

Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala 325 Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val 345 Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn 355 360 365 Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala 375 Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys 385 390 395 Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala 405 Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu 420 Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg 450 Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln 485 Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln 535 Ala Ala Gly Ile Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu 555 Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala Leu Gly Ala

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Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg
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Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
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Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
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Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr
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Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala
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547
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Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
150
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691

739

777

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Gly	Glu	Phe 115	Phe	Ala	Glu	Lys	Val 120	Leu	Arg	Lys	Phe	Glu 125	Met	Phe	Asp
Leu	Phe 130	Glu	Phe	Met	Gly	Ala 135	Ala	Thr	Asp	Ser	Gly 140	Asn	Arg	Arg	Ser
Lys 145	Ser	Ala	Val	Ile	Lys 150	His ?	Val	Leu	Asp	Ser 155	Val	Gly	Leu	Asp	Glu 160
Pro	Asn	Asp	Ile	Leu 165	Met	Ile	Gly	Asp	Arg 170	Ser	His	Asp	Ile	Glu 175	Gly
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Met Ile Lys Ala Ile

1 5

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att get acc tac gag etc age gaa gec atg gge ege ege etc acc eeg  $\,$  211 Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly Arg Arg Leu Thr Pro  $\,$  25  $\,$  30  $\,$  35

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cgc tac cgg gct ggc atg ttc gcc cgg gtc cat gag ctt ttc gac gaa 355 Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His Glu Leu Phe Asp Glu 70 75 80 85

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gcc ctc gag atc ccc atg ttg gtc acc acc aca gag cgc gat ctc 451

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105 100 110 Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu 120 Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro 135 Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro 150 155 Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala 165 Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln 185 Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile 215 Glu Pro Ala Gly Val Ala Lys <210> 639 <211> 531 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(508) <223> RXN02461 <400> 639 agaaaatctc aaggcaaaaa acaagccacc ccaatctgtg cgacaatcaa accacagact 60 acgactatta tgtcacgaag aaaccaaaga aagggaaata atg cgc gga cta att 115 Met Arg Gly Leu Ile gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163 Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg 10 tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg 211 Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val atc etc age aac gat eca ggt ggg etc gge gea geg eeg atc egg gaa 259 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu 45 ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307 Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu 60 ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355

- 915 -

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205

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ctg at Leu Il 470															1555
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								gct Ala								432
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			245					250					255		
tcc cc Ser Pr		_		_						-	_	_			816
ctg at Leu Me	-			_	_		_					_	_	-	864
cgt aa Arg Ly 29	s Lys	_					_		-	_	_		_		912
ggc ag Gly Se 305			-		_				_	_			_		960
tgg at Trp Il															1008
cct ga Pro Gl		_		_	_	_			_			_		_	1056
gat at Asp Me						-									1104
att gg Ile Gl 37	y Phe														1152
ctg at Leu Il 385	_	_	_	_	_						_		-		1200
tcc gt Ser Va		_	_			_	_		_				-	_	1248
ccc at Pro Me															1296
aag ga Lys Gl		ccat	gga t	tctca	aatao	cc tt	t								1325

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<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly

20 25 30 Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr 90 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys 185 Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His 200 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu 215 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val 235 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly 315 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn 325 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val 340 345 350

<400> 648

Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu 355 365 360 Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp 375 Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro 385 390 395 Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Pro Thr Thr Gly Glu Lys Glu <210> 647 <211> 307 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(307) <223> RXA00379 <400> 647 cgtgctggat aaacagcacc gccccgcagc agtgttcttg cgcgaagtca cctccaaaga 60 tgtgttggat gttgcgttgc cattggtaga tgaggcctaa atg tct gag att gtg 115 Met Ser Glu Ile Val gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163 Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly 10 1.5 cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211 Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser 25 259 ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr 40 45 ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307 Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr 55 60 <210> 648 <211> 69 <212> PRT <213> Corynebacterium glutamicum

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Ala	Gly	Leu 35	Val	Ser	Phe	Ala	Ser 40	Pro	Cys	Val	Val	Pro 45	Leu	Val	Pro	
Gly	Tyr 50	Ile	Ser	Tyr	Leu	Ala 55	Gly	Val	Val	Gly	Gly 60	Glu	Val	Glu	Tyr	
Ser 65	Ala	His	Ala	Thr												
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														acc Thr		96
														ggg Gly		144
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		_	_	-			_		_					ggt Gly		240
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ctc Leu	taga	iaaaa	aga d	tttt	agta	ig ga	ıa									362



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Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val 50 60

Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val 65 70 75 80

Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile 85 90 95

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Leu

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Met Asp Leu Asn Thr

1 5

ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc  $\,$  163 Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu  $\,$  10  $\,$  15  $\,$  20

gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211 Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys 25 30 35

gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259 Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp 40 45 50

gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307 Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala 55 60 65 BGI-126CP - 928 -

					tac Tyr 75										355
					gtg Val										403
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					cgt Arg										547
					ctt Leu 155			_	_		_		_	_	595
					acc Thr										643
					gct Ala										691
_		_	-	_	ctt Leu		_								739
		_	_		gca Ala			_						-	787
	_			_	gcg Ala 235	-				_		_	_		835
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<212> PRT

<213> Corynebacterium glutamicum

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220 225 215 ttc ttc gga cac cct qaq qtt tac qtt ctq qcq ctq ccq ttc ttc ggc 835 Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly 230 235 att gtt tct gag atc att cct gtg ttc tcc cgt aag cca atg ttc ggt 883 Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly tac gtc ggc ctg atc ttc gca acc ttg tcc att ggt gca ctg tcc atg 931 Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt ttg ctt ccg 979 Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val Leu Leu Pro 280 ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc ggc gtt aag 1027 Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys 295 300 ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc act tgg gaa 1075 Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu 315 acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc ctc ttc ggt 1123 Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly 330 ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac ttc cac ttg 1171 Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu 345 get gae tee tae tte etg ate geg cae tte eac tae ace ete tte ggt 1219 Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg ttc ccg aag 1267 Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc cac ttc tgg 1315 Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp 395 ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag cac tgg gtg 1363 Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val 410 415 ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg gat tct gat 1411 Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp 425 430 ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac ttc ctg ctt 1459 Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu 445 ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag tcc tgg cgc Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys Ser Trp Arg 455 460

Tyr Gly Glu 470	ctc gtt Leu Val											1555
ctg gag tgg Leu Glu Trp	_	_				_				_		1603
ttg cct cgt Leu Pro Arg	_		_					_			_	1651
cac atg att His Met Ile 520												1699
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Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro 165 Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile 185 Phe Pro Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys 195 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp 215 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val 295 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala 325 Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr 375 Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly 395 Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp 425 Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val 435 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val 455 460 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp

470

475

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Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe 505 Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro 535 Ala Leu Ala Ser Asp Ser Ser Arg 550 <210> 655 <211> 385 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(385) <223> FRXA01919 <400> 655 acctatgace getgtggege ctagggtega egggeaegte geeeeteaga ggeeegagee 60 gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac Met Thr Thr Asp cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe 10 ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr 40 45 atg cac gga act gtc atg ctg ctg tac gga act cca att gtt tgg 307 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp 55 60 ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355 Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe 70 75 80 385 tct aaa acc cgg gtg aac tct ccc agg gag Ser Lys Thr Arg Val Asn Ser Pro Arg Glu 90

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BGI-126CP

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Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Tyr Gly 50 55 60

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ctg tcc atg gct gtg gct cac cac atg ttc gtt act ggc gca gtt 163 Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val

ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr
25 30 35

ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259 Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile 40 45 50

act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe
55 60 65

ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355 Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp 70 75 80 85

ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403 Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr

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cac tgg gtg ggc a His Trp Val Gly A 150		_			_	595
gat tot gat ggt to Asp Ser Asp Gly P			-			643
ttc ctg ctt ggc c Phe Leu Leu Gly L 185	-				_	691
tcc tgg cgc tac g Ser Trp Arg Tyr G 200		_		, ,,		739
ggc aac tcc ctg g Gly Asn Ser Leu G 215			Cys Pro E	_		787
ttc gca tcc ttg cc Phe Ala Ser Leu P 230						835
cac tac ccg cac a His Tyr Pro His M 2						883
cat cac gat gat as His His Asp Asp I 265						931
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Val Thr Gly Ala Va	al Leu Leu	Pro Phe	Phe Ser E	Phe Met Thr	Phe Leu	

20 25 30 Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile 185 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro 215 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg <210> 659

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<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Corynebacterium glutamicum

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (101)..(712)

<sup>&</sup>lt;223> FRXA02481

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tgctttcggc ttctc	gaatca ccacc	gtcgg tggtgtcgcg	atg ctg acc ggc Met Leu Thr Gly 1	
			cca tgt act ccc Pro Cys Thr Pro 20	
		3 <b>3</b> 3 3	cta aca tgt gga Leu Thr Cys Gly 35	-
			gct tcc gca att Ala Ser Ala Ile 50	
<del>-</del>	_		ggt atg acc atg Gly Met Thr Met 65	
		_	gtt tcc gtt ctt Val Ser Val Leu	-
		2 2 2	ctg ggt gtt ctg Leu Gly Val Leu 100	
			gct aac ggc ggc Ala Asn Gly Gly 115	
	<del>-</del>		cac cct gag gtt His Pro Glu Val 130	
	-	22	gag atc att cct Glu Ile Ile Pro 145	
	_		cct gat ctt cgc Pro Asp Leu Arg	
			ggc tca cca cat Gly Ser Pro His 180	
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Pro Cys Thr Pro His Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val 70

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Ala Ala Ala

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser 135

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu 185

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg 200

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			-	_	_		_	_	-	gcc Ala						211
		_			_	_				gat Asp					_	259
										gtc Val						307
										ctc Leu 80						355
										gag Glu						403
_		_			-					gtt Val	_	_		_	_	451
										acc Thr						499
										gtt Val						547
-		_				_				tcc Ser 160	_		_			595
_	_				_	_				agc Ser	_	_		_	_	643
-	-	_		_		_	_	_		tct Ser		-				691
				_		-	_			ctt Leu				_		739
-						-	_			gtg Val	_	_				787
								_		gct Ala 240	-	-	-			835

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						cgt Arg										931
						cgc Arg										979
						ctt Leu 300										1027
			-		_	gac Asp				-	-			_	_	1075
						caa Gln										1123
	-		_	-		gca Ala		_	_		_			_	_	1171
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Gly	Val	Leu	Gly 20	Leu	Gly	Gly	Leu	Ala 25	Met	Ala	Gly	Cys	Glu 30	Val	Ala	
Pro	Pro	Gly 35	Gly	Val	Leu	Gly	Asp 40	Phe	Leu	Arg	Met	Gly 45	Trp	Pro	Asp	
Gly	Ile 50	Thr	Pro	Glu	Ala	Val 55	Ala	Met	Gly	Asn	Phe 60	Trp	Ser	Trp	Val	
Trp 65	Val	Ala	Ala	Trp	Ile 70	Ile	Gly	Ile	Ile	Met 75	Trp	Gly	Leu	Phe	Leu 80	
Thr	Ala	Ile	Phe	Ala 85	Trp	Gly	Ala	Lys	Arg 90	Ala	Glu	Lys	Arg	Gly 95	Glu	
Glv	Glu	Phe	Pro	Lvs	Gln	Len	Gln	Tvr	Asn	Val	Pro	Leu	Glu	Leu	Val	
			100	БуЗ	GIII	200		105		, 41			110	200	<b>V G I</b>	

Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Thr

ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct 883

115 120 125 Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val 135 140 Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser 145 150 155 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser 170 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val 215 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala 235 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp 245 250 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile 265 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp 295 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp 310 315 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala 325 Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly Glu Asn Thr Gln Ser Asn Ala 355 <210> 663 <211> 774 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(751) <223> RXA02142

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					gat Asp	_		-	-							163
					cgt Arg											211
_	-				gtg Val		_		_	-		_			_	259
					tac Tyr											307
					cag Gln 75		-							_	_	355
_		_	_		ctg Leu							_	_			403
_			_	-	agg Arg		_	-				_	-			451
_	_	_			ctc Leu								_			499
					gta Val	-						_	_	_	-	547
					ttt Phe 155											595
			_	-	gcc Ala		_		-		_	-			_	643
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Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu 35 40 45

Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala 50 55 60

Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn 65 70 75 80

Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val 85 90 95

Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly
100 105 110

Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val 115 120 125

Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr 130 135 140

Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe 145 150 155 160

His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Leu 165 170 175

Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala 180 185 190

Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly 195 200 205

Leu Phe Ile Thr Ile Tyr Phe Ile Gln 210 215

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gac aaa cag ta Asp Lys Gln Ty		_			
ctt gca cga ct Leu Ala Arg Le 2					_
aag gaa cgt tt Lys Glu Arg Ph 40	_				_
cgt gca gtt ac Arg Ala Val Th 55		Val Leu Gly I			
ttc ctg gct ac Phe Leu Ala Th 70				-	
gat gaa ggt ct Asp Glu Gly Le					
act tcc ggt ct Thr Ser Gly Le 10	u Cys Ile Leu				
gtc aag aag tt Val Lys Lys Ph 120				-	-
ggt cct tct ga Gly Pro Ser Gl 135		Arg Arg Thr I			
gac tct tgg ca Asp Ser Trp Gl 150		Leu Gly Arg A		Ile Met	
ctt gca ggt gg Leu Ala Gly Gl					
atg ggc ggt at Met Gly Gly Me 18	t Ile Lys Asn		Pro Lys Glu		
gac gtt cag gg Asp Val Gln Gl 200					_
gag aac gac gt Glu Asn Asp Va 215		Leu Gly Arg A			

					-	acc Thr				-						835
	_	_	_	_	_	cgc Arg		_	_	_	-	_	_		_	883
						cca Pro										931
						gtc Val										979
						atg Met 300					-		_	_	_	1027
						gaa Glu										1075
						att Ile										1123
_			_	_		aat Asn	_		_			_		_	_	1171
						tac Tyr				_				-	-	1219
_	_	_		-	_	cca Pro 380			_	_	_					1267
						att Ile										1315
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Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu 65 70 75 80

Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr 85 90 95

Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe 100 105 110

Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val 115 120 125

Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile 130 140

Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg 145 150 155 160

Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu 165 170 175

Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro 180 185 190

Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser 195 200 205

Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp 210 215 220

Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp 225 230 235 240

Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu 245 250 255

Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val 260 265 270

Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln 275 280 285

Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu 290 295 300

Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser 305 310 315 320

Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile 325 330 335

Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys 340 345 350

Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val

355 360 365 Phe Gly Pro Ala Ala Arq Ala Leu Pro Gln Leu Pro Ile Thr Val Asp 375 Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly 385 390 Pro Ala Phe Trp Glu Arg Lys Ser <210> 667 <211> 1053 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1030) <223> RXA02740 <400> 667 aacgcaaggt gcacactcac cgcagggata tttaaataat aaggactcac aacttaaata 60 tatgagtgat ttgaaaatgc aacgttctgg aggagaaccc ttg gac acg atc aag Leu Asp Thr Ile Lys gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc 163 Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Val 10 gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211 Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile gtg etc atc ttg etg act gtg tte ggt gge tgg atg ggt gee gee 259 Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307 Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met gga ege act agg get ege eet ttg gtg ege eac ace gtg agt aat ege 355 Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403 Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp 90 95 . 100 ctg tgg ctg tgc gat tcg atg ctc gcc ggc atc ttc gtg ttg atc 451 Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile 105 110 115 acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499 Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg 120 125

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ctc Leu 150	gtc Val	ggc Gly	tgg Trp	gca Ala	gtg Val 155	atc Ile	gtt Val	gat Asp	cag Gln	ttt Phe 160	gag Glu	cca Pro	ggc Gly	gtt Val	cca Pro 165	595
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atc Ile	aaa Lys	aac Asn	ggt Gly 265	ggc Gly	aag Lys	gtc Val	aag Lys	cct Pro 270	ctg Leu	aag Lys	ctg Leu	ttt Phe	att Ile 275	ttg Leu	tcc Ser	931
													gac Asp			979
ctc Leu	ggc Gly 295	Leu	gag Glu	acc Thr	atc Ile	300 ggc	Glu	atg Met	ctc Leu	ggc	tgg Trp 305	acc Thr	acc Thr	acc Thr	ttc Phe	1027
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Glu	Leu	Leu	Leu 20		Ala	Thr	Ile	Pro 25		Met	Leu	Gln	Ala 30		Arg	

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Met Gly Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp 50 55 60

Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His 65 70 75 80

Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val
85 90 95

Ala Ser Phe Leu Trp Leu Trp Leu Cys Asp Ser Met Leu Ala Gly 100 105 110

Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys
115 120 125

Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala 130 135 140

Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe 145 150 155 160

Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met 165 170 175

Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys 180 185 190

Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val 195 200 205

Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala 210 215 220

Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr 225 230 235 240

Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile 245 250 255

Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys 260 265 270

Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu 275 280 285

Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly 290 295 300

Trp Thr Thr Thr Phe Phe 305 310

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Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser

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200 205 210 787 atc acc atg gat gat egc etc gat gtc agc atc gac ttg atg gcc cac Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile Asp Leu Met Ala His 215 220 225 atc cac ggc tac agc atg tac atc tac ctc ttc ttc acc ctc atc gtg 835 Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val 230 235 Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu 250 ggc ctc atg ctg att ctg ttc att ctg att cag gca ggt atc ggc atc 931 Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile 265 979 ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile 280 gca atg tot tot gto gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag 1027 Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln 295 300 ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat 1075 Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp 315 ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca 1123 Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser 330 aag cag cct gtt aaa taacacgcaa ctgtatcggt aaa 1161 Lys Gln Pro Val Lys 345 <210> 670 <211> 346 <212> PRT <213> Corynebacterium glutamicum <400> 670 Val Ser Thr Ser Asp Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val 40 Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln

70

Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala

85 90 95 Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Glu 100 105 Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala 115 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val 135 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile 150 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu 185 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His 200 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile 215 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe 230 235 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln 265 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser Lys Gln Pro Val Lys 340 <210> 671 <211> 444

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Corynebacterium glutamicum

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (101)..(421)

<sup>&</sup>lt;223> RXA01227

BGI-126CP - 954 -

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acci	tatti	ttc (	cacg	tctt	ta to	ccgta	agta	t tg	gaga	tccg	_				atc Ile. 5	115
					gat Asp											163
					tac Tyr											211
					tgc Cys											259
					gat Asp											307
	-		-	-	ttt Phe 75		_	_			_				-	355
_	_	_		_	cag Gln	_		_	_	_		_			_	403
_		cag Gln		_	aac Asn	tago	gacci	tga 1	tato	ggcc	ct aa	aa				444
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Cys	Val	Glu	Glu 20	Cys	Pro	Val	Asp	Cys 25	Ile	Tyr	Glu	Gly	Lys 30	Arg	Met	
Leu	Tyr	Ile 35	His	Pro	Asp	Glu	Cys 40	Val	Asp	Cys	Gly	Ala 45	Cys	Glu	Pro	
Val	Cys 50	Pro	Val	Glu	Ala	Ile 55	Phe	Tyr	Glu	Asp	Asp 60	Val	Pro	His	Glu	
Trp 65	Trp	Asp	Tyr	Thr	Gly 70	Ala	Asn	Ala	Ala	Phe 75	Phe	Asp	Asp	Leu	Gly 80	
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25

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro 35 40 45

Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu 50 55 60

Trp Leu Asp Tyr Asn Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly 65 70 75 80

Ser Pro Gly Gly Ala Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro 85 90 95

Met Ile Ala Ala Leu Pro Pro Gln Ala 100 105

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ttc att gat cat gct ggc aaa acc cgc acc atc gag gcg act gtt ggt 163 Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile Glu Ala Thr Val Gly 10 15 20

gat tca gta atg gag acc gca gtc cga aac gga gtg cct gga att gtt 211 Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly Val Pro Gly Ile Val 25 30 35

gct gaa tgc ggc ggt tcc tta tcg tgt gca acc tgc cat gtg ttt gtt 259 Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr Cys His Val Phe Val 40 45 50

gac cct gca cag tat gat gcg ctt ccc cca atg gag gag atg gaa gat 307
Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met Glu Glu Met Glu Asp
55 60 65

gaa atg ctg tgg ggt gct gcc gtg gac cgt gag gat tgc tcc cgt ttg 355 Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu Asp Cys Ser Arg Leu 70 75 80 85

tct tgc caa atc aag gtc acc gaa ggc atg gat ctt tcg ttg acc acg
Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp Leu Ser Leu Thr Thr
90 95 100

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Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr
Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met
Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu
Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp
Leu Ser Leu Thr Thr Pro Glu Thr Gln Val
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                                                                   115
                                            Met Asn Thr Ser Ala
gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg
                                                                   163
Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu
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                                     15
gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta
                                                                   211
Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu
                                 30
ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag
                                                                   259
Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu
         40
                             45
ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat
                                                                   307
Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn
                         60
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							att Ile								355
							gac Asp								403
							cgt Arg								451
							ggc Gly 125								499
_	_			_	-	_	ttg Leu					_			547
							ggt Gly								595
	_	_			_		ggc Gly			_		_	_	_	643
	_	-	_			_	gcg Ala			_	_		-	-	691
							cgt Arg 205								739
-	_		_				aag Lys	_		_		_			 787
					-		cct Pro	_			_				835
							ctt Leu								883
							aaa Lys				-		-		931
					_	-	gcc Ala 285								 979
				-	_		cga Arg		_	_	_			-	1027

		_	_	atc Ile	-	-				-		_	_	_	1075
	-			ccc Pro 330								_			1123
		-		ctt Leu					-	-		-	_	_	1171
_				aag Lys	_			_				_	 _		1219
		-	_	gat Asp	_	_		_		_	_		 _	, ,	1267
				tcc Ser											1315
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cga Arg	tgad	ctcg	cag t	caatt	taco	cc go	et								1389

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<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

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Ser Gly Val Gln Leu Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu 20 25 30

Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro 35 40 45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu 50 60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val 65 70 75 80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly 85 90 95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu 100 105 110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu

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Glu	Gly 130	Val	Thr	Tyr	Leu	Arg 135	Asn	Ala	Asp	Asp	Ala 140	Leu	Ala	Leu	Ly
Ala 145	Met	Ile	Gly	Ser	Val 150	Thr	Asp	Ala	Val	Val 155	Val	Gly	Gly	Gly	Phe 160
Ile	Gly	Leu	Glu	Ala 165	Ala	Cys	Ser	Leu	His 170	Asp	Leu	Gly	Lys	Asn 175	Va.
Thr	Val	Leu	Glu 180	Tyr	Gly	Pro	Arg	Leu 185	Ile	Gly	Arg	Ala	Val 190	Gly	Glı
Glu	Thr	Ala 195	Ala	Phe	Phe	Leu	Glu 200	Gln	His	Arg	Ser	Arg 205	Gly	Val	Ası
Ile	Val 210	Leu	Asp	Ala	Arg	Met 215	Lys	Gln	Phe	Val	Gly 220	Lys	Asp	Gly	Lys
Leu 225	Ser	Gly	Ile	Glu	Leu 230	Glu	Asp	Gly	Thr	Val 235	Ile	Pro	Ala	Gln	Let 240
Val	Ile	Val	Gly	Ile 245	Gly	Val	Ile	Pro	Asn 250	Thr	Glu	Leu	Ala	Ala 255	Val
Leu	Gly	Leu	Asp 260	Ile	Asn	Asn	Gly	Ile 265	Val	Vał	Asp	Lys	His 270	Ala	Val
Ala	Ser	Asp 275	Gly	Thr	Thr	Ile	Ala 280	Ile	Gly	Asp	Val	Ala 285	Asn	Ile	Pro
Asn	Pro 290	Ile	Pro	Gly	Ser	Pro 295	Ala	Asp	Glu	Arg	Ile 300	Arg	Leu	Glu	Sei
Val 305	Asn	Asn	Ala	Ile	Glu 310	His	Ala	Lys	Ile	Ala 315	Ala	Tyr	Ser	Leu	Val 320
Gly	Gln	Pro	Glu	Ala 325	Tyr	Ala	Gly	Ile	Pro 330	Trp	Phe	Trp	Ser	Asn 335	Glr
Gly	Asp	Leu	Lys 340	Leu	Gln	Ile	Ala	Gly 345		Thr	Leu	Gly	Tyr 350	_	Ser
Thr	Val	Ile 355	Arg	Gln	Asp	Pro	Glu 360	Lys	Lys	Lys	Phe	Ser 365	Val	Leu	Туг
Tyr	Arg 370	Gly	Asp	Asn	Ile	Ile 375	Ala	Ala	Asp	Cys	Val 380	Asn	Ala	Pro	Leu
Asp 385	Phe	Met	Ala	Val	Arg 390	Ser	Ala	Leu	Ser	Arg 395	Asn	Gln	Asn	Ile	Pro 400
Ala	Asp	Leu	Ala	Ala 405	Asp	Ile	Ser	Gln	Pro 410	Leu	Lys	Lys	Leu	Ala 415	Val
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                                                                   115
                                             Met Ser Ile Ser Tyr
gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa
                                                                   163
Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu
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ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt
                                                                   211
Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val
ggc gag cca ggt gcc ggc gta aac ctt gct gag ctc ggc aat tgg
                                                                   259
Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp
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ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt
                                                                   307
Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg
ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac
                                                                   355
Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn
70
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cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct
                                                                   403
Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala
ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc
                                                                   451
Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val
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gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc
                                                                   499
Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr
att cag gtg too got goa gtt ggt ggc got toa cog ctg tac acc ctg
                                                                   547
Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu
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cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg
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Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu
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                                        160
gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc
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Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr
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tcc ttc acg cca agc acc cag agc gat cqc cct gag ctg cca cag qca
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cgc agc at Arg Ser II 215														787
gca acc co Ala Thr An 230		-	_	-	_								-	835
gtt ggt ca Val Gly G	_		_					_						883
ggc att to Gly Ile Se		_		_					_			_	_	931
aag gtt at Lys Val II 28														979
gcg gac ct Ala Asp Le 295														1027
atc,gaa ga Ile Glu G 310						tago	gagtt	itt ç	gaaca	acttt	t ta	at		1074
Ile Glu G	lu Ile	Asn	Lys 315	Arg	Lys		gagtt	ctt o	gaaca	ectt	et ta	at		1074
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The Glu Grant   State   Stat	lu Ile ynebact	Asn	Lys 315 um gl	Arg	Lys	ı							Glu	1074
The Glu Grant   The Glu Grant	lu Ile ynebact Le Ser	Asn ceriu Tyr 5	Lys 315 um gl Val	Arg Lutam	Lys nicum Val	ı Glu	Gln 10	Leu	Asp	Gly	Arg	Pro 15		1074
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100 105 110 Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser 120 Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser 130 135 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro 185 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu 215 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr 235 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp 250 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly 265 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys <210> 681 <211> 909 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(886) <223> RXA00225 <400> 681 gtaggcgtcg aaaagcaatg ggcgaagccc gcgtagtatg ggcgggcaac gctaaaagcg 60 ccaaaaacgc caaaaatcgt gaattgaaag gtgagtgtgg atg tcc aca atc gtg 115 Met Ser Thr Ile Val 1 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu

20 10 15 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu 25 atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac 259 Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 40 ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt 307 Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca 355 Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc 403 Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr 90 get tgg geg etg aac aac get atc aac acc atc geg ggt gtt get etc 451 Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu 105 ate gtg acg ggt teg get tet tee gat ggt tee atg ggt geg ett eet 499 Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro 120 ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct 547 Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac 595 Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile 170 tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg 691 Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met 190 gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc 739 Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly 205 gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act 787 Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr 220 gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca 835 Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala 235 240 tog ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc 883 Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu 250

atc tagccactat cttcacaaag gag

909

<210> 682

<211> 262

<212> PRT

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<400> 682

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Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg 35 40 45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser 50 55 60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met 65 70 75 80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser 85 90 95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile 100 105 110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser 115 120 125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala 130 135 140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala 145 150 155 160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro 165 170 175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn 180 185 190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser 195 200 205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala 210 215 220

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Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu 245 250 255

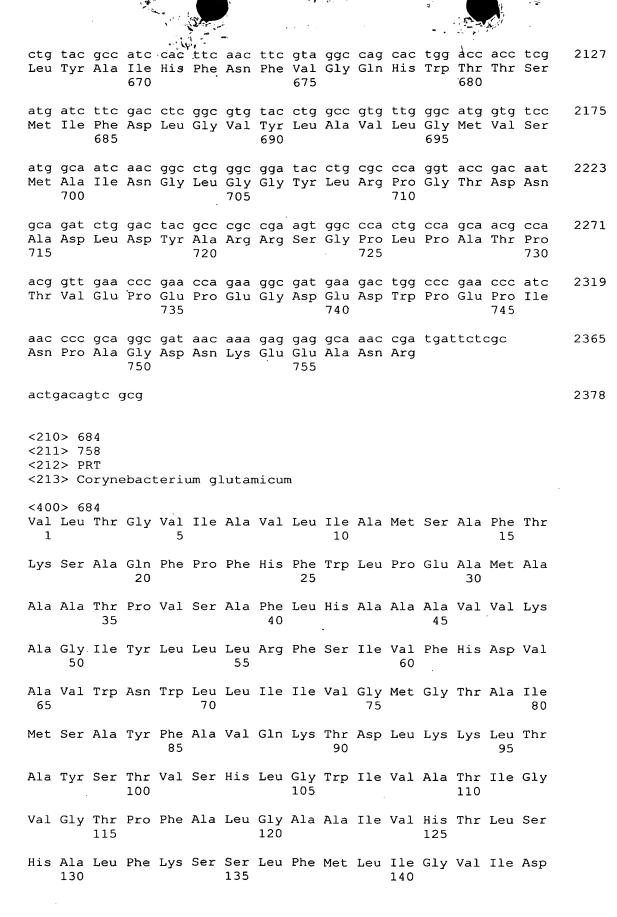
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gca atg tcc gcg ttc act aag tcc gca cag ttc ccg ttc cac ttc tgg 15 Ala Met Ser Ala Phe Thr Lys Ser Ala Gln Phe Pro Phe His Phe Trp 15 20 25	.59												
etg cet gag geg atg get geg gee ace eea gtg teg geg tte etg eac 20 deu Pro Glu Ala Met Ala Ala Ala Thr Pro Val Ser Ala Phe Leu His 30 35 40	:07												
get geg gee gtg gte aag geg ggt att tae etg ttg etg ege ttt age 25 Ala Ala Ala Val Val Lys Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser 45 50 55	:55												
att gtg ttc cat gat gtt gcg gtc tgg aat tgg ttg ctg att atc gtc 30 Tle Val Phe His Asp Val Ala Val Trp Asn Trp Leu Leu Ile Ile Val 60 65 70	03												
ggc atg ggt acg gcc atc atg tcg gcg tat ttc gcg gtg cag aag acc 35 Gly Met Gly Thr Ala Ile Met Ser Ala Tyr Phe Ala Val Gln Lys Thr 75 80 85 90	51												
gat ctg aag aag ctc acg gca tat tcc acg gtg tcg cat ttg ggt tgg 39 Asp Leu Lys Lys Leu Thr Ala Tyr Ser Thr Val Ser His Leu Gly Trp 95 100 105	99												
tc gta gcg acc atc ggc gtg ggc act cct ttc gcg ctc ggc gct gcc 44 le Val Ala Thr Ile Gly Val Gly Thr Pro Phe Ala Leu Gly Ala Ala 110 115 120	47												
tt gtg cac acg ctc agc cac gcg ctg ttt aag tcc tcg ttg ttc atg 49 Tle Val His Thr Leu Ser His Ala Leu Phe Lys Ser Ser Leu Phe Met 125 130 135	95												
etc att ggc gtg att gat cac cag act ggc acg cgc gat att cgt cgc 54 eu Ile Gly Val Ile Asp His Gln Thr Gly Thr Arg Asp Ile Arg Arg 140 145 150	43												
etc ggt ttc ctg gtc aag aag atg ccg ttc acg ttt gtg tct gta tta 59 eu Gly Phe Leu Val Lys Lys Met Pro Phe Thr Phe Val Ser Val Leu 55 160 165 170	91												
ta ggt gcg ttg tcg atg gca tcg gtt ccg ccg ttg ctc ggc ttc gtg 63	39												

Ile	Gly	Ala	Leu	Ser 175	Met	Ala	Ser	Val	Pro 180	Pro	Leu	Leu	Gly	Phe 185	Val	
								ttc Phe 195								687
		-	_		_	_	-	ggc Gly	_	_				_		735
								gtg Val								783
	_	_	_			_	_	gaa Glu	_		_					831
_	-	-	_				_	tct Ser	_			_		-		879
								gcc Ala 275								927
_				_		_	_	ttg Leu								975
								gtg Val								1023
	_			_				gcc Ala			_					1071
		Gly	Asn	Asp	Ile	Leu	Ser	atg Met	Leu	Val	Tyr	Arg	Āla			1119
								gct Ala 355								1167
	_	_	_				_	ctc Leu			_	-	-		_	1215
				_	_	-		gca Ala		_		_			-	1263
								gcc Ala								1311
								ctc Leu								1359

415 420 425

acc gtt ggt gtg ggt gtt tcc ttc cag atg cta ctt ctg ggc gct ccc 1407 Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Gly Ala Pro 430 435 gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc 1455 Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile atc atg atg gtt gtc cgg cac cag cct gcc aac ttc aag cgc atc aag 1503 Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys 460 ccc age aga agg cgc age acc gtt ctt gtc gcc gtc ctt gct gcc ttc 1551 Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe 475 480 gcc gca ttc atg gcg gtg tgg gga ttg ctt ggc cgt cac gaa cgt tct 1599 Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser 495 gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc 1647 Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly 510 gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg 1695 Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr 525 ttg ggc gag ctc tcc gtg ctt ggc atg gca gct gtc gtc atc ggt gcg 1743 Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala 540 atg gtg gct tcc atg cct cgt cat ccg ttt gcc aag ggc acc cac cct 1791 Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu 575 ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc 1887 Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe 595 atg cgt gga cac aat gat ccg gga ggc ggt ttc atc gca gcc cta att 1935 Met Arg Gly His Asn Asp Pro Gly Gly Phe Ile Ala Ala Leu Ile 610 gcc ggt ggc gcg ctg atg ctc ctg tac ctg tcc aag gcc aaa gat ggc 1983 Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly 625 ege att tte ege eeg aat gtt eet tte att ete act ggt geg gge ate 2031 Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile 640 645 ttg atg gca gtg ttc tcg ggc gta ctg gga ctc acc cac ggt tct ttc 2079 Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe 655 660



į



His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys 150 155 Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala 215 Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His 225 235 Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro 265 Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile 390 395 Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg 405 410 Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val 425 Ser Phe Gln Met Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln 435 440 Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val Arg 455 His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser



465 470 475 480 Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val 485 490 Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr 505 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser 565 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Lys Val Leu Val Pro 585 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp 600 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met 615 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn 635 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe 665 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu 695

Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala

Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro 725 730 735

Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn 740 745 750

Lys Glu Glu Ala Asn Arg 755

<210> 685

<211> 1872

<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1849)
<223> FRXA00606

185

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	ctg Leu															739
_	caa Gln 215	_			_	_			_			_		_		787
	gcg Ala			_			_				-		_		_	835
	gcc Ala															883
	ctt Leu	_		_		_	_				_		_	-		931
	ctc Leu	_		_			_	_	_	_			_		-	979
	ttc Phe 295	_	-		-		_	_		-	_		-		_	1027
	gtc Val															1075
	cgt Arg															1123
	gag Glu					_									-	1171
	cgt Arg															1219
	gtc Val 375															1267
_	aag Lys					-							_			1315
	ccg Pro															1363
_	agc Ser		_			_	-				_	_				1411
ttc	atc	gca	gcc	cta	att	gcc	ggt	ggc	gcg	ctg	atg	ctc	ctg	tac	ctg	1459

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Phe	Ile	Ala 440	Ala	Leu	Ile	Ala	Gly 445	Gly	Ala	Leu	Met	Leu 450	Leu	Tyr	Leu	
	_	-		_		cgc Arg 460			_	_		_				1507
						ttg Leu	_				-		_	_		1555
						ctg Leu										1603
						atg Met										1651
						atg Met										1699
						gca Ala 540										1747
						acg Thr	-			-		_		_	-	1795
-			-			aac Asn		_		_					_	1843
aac Asn	_	tgat	tctc	cgc a	ctga	acagt	c go	g								1872

<210> 686

<211> 583

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met

Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu

Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser 40

Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser 55

His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro 70 75

Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala 85 Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met 100 105 His Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu 120 Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu 135 Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr 230 235 Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Gly Ala Pro Asp Val Ala Leu Thr 265 Gln Phe Leu Val Glu Gly Leu Val Val Ile Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser 360 Val Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met 370 375

Pro Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln

Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val

395

390

				405					410					415		
Prọ	Ala	Leu	Cys 420	Phe	Leu	Ser	Phe	Met 425	Val	Phe	Met	Arg	Gly 430	His	Asn	
Asp	Pro	Gly 435	Gly	Gly	Phe	Ile	Ala 440	Ala	Leu	Ile	Ala	Gly 445	Gly	Ala	Leu	
Met	Leu 450	Leu	Tyr	Leu	Ser	Lys 455	Ala	Lys	Asp	Gly	Arg 460	Ile	Phe	Arg	Pro	
Asn 465	Val	Pro	Phe	Ile	Leu 470	Thr	Gly	Ala	Gly	Ile 475	Leu	Met	Ala	Val	Phe 480	
Ser	Gly	Val	Leu	Gly 485	Leu	Thr	His	Gly	Ser 490	Phe	Leu	Tyr	Ala	Ile 495	His	
Phe	Asn	Phe	Val 500	Gly	Gln	His	Trp	Thr 505	Thr	Ser	Met	Ile	Phe 510	Asp	Leu	
Gly	Val	Tyr 515	Leu	Ala	Val	Leu	Gly 520	Met	Val	Ser	Met	Ala 525	Ile	Asn	Gly	
Leu	Gly 530	Gly	Tyr	Leu	Arg	Pro 535	Gly	Thr	Asp	Asn	Ala 540	Asp	Leu	Asp	Tyr	
Ala 545	Arg	Arg	Ser	Gly	Pro 550	Leu	Pro	Ala	Thr	Pro 555	Thr	Val	Glu	Pro	Glu 560	
Pro	Glu	Gly	Asp	Glu 565	Asp	Trp	Pro	Glu	Pro 570	Ile	Asn	Pro	Ala	Gly 575	Asp	
Asn	Lys	Glu	Glu 580	Ala	Asn	Arg										
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<222	l> CE 2> (1 3> RX	01).		530)												
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ttca	agtca	icc a	acco	caaca	ig at	cago	agga	a taa	agct	taa		gcc Ala				115
	ctt Leu															163
	ctt Leu															211

							ggc Gly 45									259
					Ala		aac Asn									307
							acg Thr									355
							gcc Ala									403
-		-		_			cca Pro	-			_	-	_		_	451
	-			_	_	_	act Thr 125	_	_	_						499
		_		_	_	_	cct Pro				_		_	_		547
							tct Ser									595
							gtt Val									643
							gca Ala									691
		_	-	_	_	-	atg Met 205				_		-			739
							gtg Val									787
							atg Met									835
							tat Tyr	-								883
							ctg Leu									931
atg	ctg	gtc	ggt	ggc	ttc	gct	gga	ctt	gct	gaa	aac	tcc	atc	cgt	cgc	979

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Met	Leu	Val 280	Gly	Gly	Phe	Ala	Gly 285	Leu	Ala	Glu	Asn	Ser 290	Ile	Arg	Arg	
	ctt Leu 295															1027
	gcg Ala															1075
_	tac Tyr		_			_				_	_	_				1123
	ggc Gly	_		_	_						_	_		_	_	1171
	ggc Gly		-	_	-	_		_	-	_	_			-	-	1219
	gcc Ala 375			•	_				_				-			1267
	gcg Ala															1315
	atc Ile	_			_				_	_	_		-	_		1363
	atg Met		_			_	_	_					_	_		1411
_	cgc Arg		Val	_	-	Gln	_	Arg		_	Pro	_	Lys		_	1459
	gcg Ala 455															1507
	ccg Pro			_					_		_			_		1555
	gat Asp															1603
	agc Ser								taat	gctt	caa d	egeed	ctgaa	aa		1650
ttc																1653

<210> 688

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 688

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala 1 5 10 15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile 20 25 30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu 35 40 45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu 50 55 60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala 65 70 75 80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe 85 90 95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr 100 105 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu 115 120 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly 130 135 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile 145 150 155 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
165 170 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln 180 185 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val 195 200 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp 210 215 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe 225 230 235 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp 245 250 255

Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala 260 265 270

Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu 275 280 285 Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro 295 Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala 305 315 Leu Ala Ala Gly Leu Leu Tyr Thr Leu His His Met Ile Thr Ile Ala Ala Leu Val Leu Thr Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly Met Leu Ser Lys Leu Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala Ala Val Phe Ala Ala Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe 375 Ser Gly Met Trp Gly Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val 390 395 Gly Asn Ile Ala Ala Trp Ile Ala Ile Ala Ile Ile Ile Ala Ser 410 Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp 425 Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly 455 Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr 470 475 Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn 505 <210> 689 <211> 865 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(865) <223> FRXA00608 <400> 689

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163

cgacgacacc cggtccatcg aaccagatga cgatcaatcg cctttgacta ctagcgctcg 60

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg

Leu	Leu	Pro	Ile	Phe 10	Val	Ala	Val	Pro	Leu 15	Ala	Ala	Ser	Ala	Ile 20	Ala	
					cgt Arg											211
					ttt Phe											259
					gct Ala											307
					gcc Ala 75											355
	_		_		gtg Val	_	_				_			_		403
					ttc Phe											451
	-			_	ctg Leu	_		_	_	_						499
		-		_	ctg Leu	_					_		_	_		547
	_			_	cta Leu 155	_			_			_		_		595
					ttg Leu											643
_				_	aac Asn		_	_	_		-	_	_			691
					agc Ser											739
					ttc Phe											787
					gct Ala 235											835
					atg Met											865

250 255

<210> 690

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala 1 5 10 15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile 20 25 30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu 35 40 45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu 50 55 60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala 65 70 75 80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe 85 90 95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr 100 105 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu 115 120 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly 130 135 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile 145 150 155 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val 165 170 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln 180 185 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val 195 200 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp 210 215 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe 225 230 235 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile 245 250 250

<210> 691

<211> 2118

<212> DNA

BGI-126CP - 983 -

<213> Corynebacterium glutamicum

<220> <221> CDS

<222> (1)..(2118)

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						tcc Ser									96
	-		_	_		acc Thr 40				_	_		_		144
						caa Gln			-		_	_	_	_	192
-	_			_	Āla	ggt Gly		_		_					240
						acc Thr									288
						ctg Leu									336
		_	_		_	tac Tyr 120		_		_	-		-	_	384
						gcc Ala									432
						aag Lys									480
						ggt Gly									528
_		_	_		_	aac Asn	-	_		_		-	_	-	576
						cat His 200									624

tct gtg gtg atc atc att tcc gga ttc atc ttc tgg gag cga gac 672

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Ser	Val 210	Val	Ile	Ile	Ile	Ser 215	Gly	Phe	Ile	Ile	Phe 220	Trp	Glu	Arg	Asp	
	-	_	_	_	_		aac Asn		_				-	-	-	720
	_		_	-			gat Asp	_	_	_					_	768
							ggt Gly									816
							gtt Val 280									864
							gag Glu									912
							gtc Val									960
							att Ile								ggc Gly	1008
	_	_					cat His		_	_	-	_				1056
							gtc Val 360									1104
_		-	_		_	_	gcg Ala		_	Āla	_			_		1152
							ggc Gly									1200
							gct Ala									1248
							gag Glu									1296
							cgt Arg 440									1344
							acc Thr									1392

450 455 460 aac ege age tte ege aag gat tet ege aga eea ace etg get ace act 1440 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr 470 ggt cgc cgt tgg ttg gct gct gtt gat acc gaa agg gcg cag aac 1488 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn 485 cgc tcg ctg atg gtt gat gtg gca acg cgc atc ctc ttc cct gcc atg 1536 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met ate atg ttg tet gtg tac tte tte tee gee gga cae aac geg eeg gge 1584 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly 515 gge gga tte gee gge gge ett gtt gee tee ttg geg tte gee ttg ege 1632 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arq 530 tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac 1680 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp 545 gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg 1728 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att 1776 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile 580 tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg 1824 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala 595 ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg 1872 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met cac att ctc aac agt ttg ggc ggc cag ctc gac cqc gat gag gaa atg 1920 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag 1968 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Leu Ala Arg Asn Gln cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg 2016 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser 665 aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg 2064 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser 680 gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu 695 700

2118

aag cag Lys Gln 705

<210> 692 <211> 706

<212> PRT

<213> Corynebacterium glutamicum

<400> 692

Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys 35 40 45

Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala 50 55 60

Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile 65 70 75 80

Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
85 90 95

Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile 100 105 110

Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr 115 120 125

Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu 130 135 140

Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu 145 150 155 160

Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu 165 170 175

Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val 180 185 190

His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu 195 200 205

Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp 210 215 220

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp 225 230 235 240

Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg 245 250 255

Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val

260 265 270 Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly 280 Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly 295 Phe Ile Ala Ala Ile Ile Val Val Ala Ile Val Ala Thr Thr Met Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr Gln Val Leu Val Glu Thr Ile Val Met Val Phe Met Leu Val Leu Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser 375 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg 455 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr 475 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly 520 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg 535 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp 555 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val 565 570 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile 580 585

Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala 595 600 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met 615 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met 625 635 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu 695 Lys Gln 705 <210> 693 <211> 955 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(955) <223> RXA00909 <400> 693 tegatgtgtg ttgctaactg ggggtggcac gcacgttggc gttgttgttt ggtgtggctc 60 cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt 115 Val Leu Ile Leu Phe ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163 Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr 10 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly 25 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly 40 45 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307 Gly Glu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn 55 60 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val

70					75					80				85	
				-		_	ctg Leu	-		_				_	403
							gcc Ala								451
							gtc Val 125								499
	_			-			tcc Ser	_				_	_		547
			_	-	_		tca Ser	_	-		_		_	_	595
							ttg Leu								643
							tgg Trp								691
							ccg Pro 205								739
							aaa Lys								787
							gca Ala								835
							gcg Ala								883
		_			_	-	ggt Gly	-			_			_	931
_		_	_	acc Thr	_		_								955
	)> 69 L> 28														

<211> 285 <212> PRT

<213> Corynebacterium glutamicum

<400> 694

BGI-126CP - 990 -

Val Leu Ile Leu Phe Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala 105 Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser 135 Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr Ser Ser Srr Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile 215 Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met 280

<sup>&</sup>lt;210> 695

<sup>&</sup>lt;211> 927

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Corynebacterium glutamicum

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200 205 210 ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc 787 Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe 215 220 225 835 acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta Thr Ser Val Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu 230 235 cga cgc gcc agc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg 883 Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly 250 gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc 927 Glu Ala Gly Val Pro Arg Val 265 <210> 696 <211> 268 <212> PRT <213> Corynebacterium glutamicum <400> 696 Met Ile Asn Ala Ile Thr Leu Lys Pro Lys'Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Gly Phe Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro 105 Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu 115 120 Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala 135 Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys 145 150 155 160 Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly 170 Tyr Gly Thr Met Met Asn Met Ser Phe Trp.Pro Tyr Ala Ile Gly Val 180 185

Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
195 200 205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu 210 215 220

Gly Arg Ala Phe Phe Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro 225 230 235 240

Val Leu Gly Ala Leu Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val 245 250 255

Glu Arg Asp Phe Gly Glu Ala Gly Val Pro Arg Val 260 265

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<211> 1587

<212> DNA

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<223> RXN00483

<400> 697

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teccaetttg cattateaag eteaaaacee geaeeggega gtg etg gte ace ggt 119 Val Leu Val Thr Gly 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc  $\,$  163 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala  $\,$  10  $\,$  15  $\,$  20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg 25 30 35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac  $\phantom{0}$  259 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp  $\phantom{0}$  40  $\phantom{0}$  45  $\phantom{0}$  50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile 105 110 115

							cgc Arg 125									499
							gct Ala									547
							ttt Phe									595
							cct									643
		_			-	-	ttg Leu					_		_	_	691
		_		_		-	tcc Ser 205	_	-			_		_	_	739
				-		_	cgt Arg			_	_	-			_	787
	_		-			-	cct Pro			_		_	-	_		835
							gtg Val									883
							gct Ala	_			_		_			931
							gat Asp 285									979
							tta Leu									1027
							tgg Trp									1075
							gcg Ala									1123
							cga Arg	_		_	_		_			1171
gaa	ggt	ttg	ggt	ggc	gtg	aac	ggc	tgg	tat	tct	gca	сса	ctg	cta	tgg	1219

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Glu	Gly	Leu 360	Gly	Gly	Val	Asn	Gly 365	Trp	Tyr	Ser	Ala	Pro 370	Leu	Leu	Trp	,
											ggt Gly 385					1267
											gat Asp					1315
		_				-				_	tta Leu				_	1363
			-	-			_		_		ctg Leu	_	-		_	1411
											gca Ala					1459
_		_								_	gtt Val 465		_			1507
						_	_				tta Leu		_		_	1555
	ctc Leu		taat	cgca	aga g	gtago	gcgto	ct aa	aa							1587
<211 <212	0> 69 L> 48 2> PF 3> Co	38 RT	ebact	eri	ım gl	utan	nicum	α								
	)> 69 Leu	-	Thr	Gly 5	Ala	Thr	Gly	Tyr	Ile 10	Gly	Gly	Arg	Leu	Ile 15	Thr	
Glu	Leu	Leu	Ala 20	Ala	Gly	Phe	Gln	Val 25	Arg	Ala	Thr	Ser	Arg 30	Lys	Lys	
Thr	Ser	Leu 35	Gln	Arg	Phe	Asp	Trp	Tyr	Glu	Asp	Val	Glu	Ala	Val	Glu	

40 45 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro

100 105 110 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu 120 Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu 135 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile 150 155 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile 165 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu 235 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala 265 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu 295 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly 390 395 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg 405 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile 420 425

Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
435 440 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val 450 455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr 485

<210> 699

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> FRXA00483

<400> 699

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teceaetttg cattateaag eteaaaeee geaeeggega gtg etg gte ace ggt 115 Val Leu Val Thr Gly 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gcc 163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
10 15 20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc  $\,$  211 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg  $\,$  25  $\,$  30  $\,$  35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile

120 125 130 ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547 Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile 135 140 att ggt tee gge tet gea tea ttt gaa ata ate egt eat ete aeg gag 595 Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu 150 155 cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat 691 Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 185 190 tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg 739 Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser 200 tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg 787 Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu 215 220 aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta 835 Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 tee ggt ett tgg att agt eta gtg aca eet gtt eea ttt eaa ttg tet 883 Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser 250 ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac 931 Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 age att aaa gat att att tea gat eee eee gat ggt tit att gag tat 979 Ser Ile LysrAsp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt 1027 Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val 295 300 cca acq tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc 1075 Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly 310 cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc 1123 Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att 1171 Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile 345 350 gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg 1219 Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp 365

_	_				_	_	_							ttg Leu		1267
			_		_		_				-	_		gat Asp		1315
		-		_		-				_				acc Thr 420	_	1363
	_		_	_			_		_		_	_	_	gcg Ala	_	1411
_	-				-				_	_	_			gag Glu	_	1459
														ttc Phe		1507
						_	_	_					_	gcg Ala	-	1555
	ctc Leu		taat	cgca	aga g	gtago	gcgto	ct aa	aa							1587
	)> 70 .> 48	-														
	.> 48 2> PF															

<213> Corynebacterium glutamicum

<400> 700

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro 100 105 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu 130 135 140

Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile 145 150 155 160

Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile 165 170 175

Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu 180 185 190

Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile 195 200 205

Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala 210 215 220

Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu 225 230 235 240

Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val 245 250 255

Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala 260 265 270

Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp 275 280 285

Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu 290 295 300

Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln 305 310 315 320

Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala 325 330 335

Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln 340 345 350

Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser 355 360 365

Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly 370 375 380

Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly 385 390 395

Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg 405 410 415

Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile 420 425 430

Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg

435

445

440

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547

589

612

ttc ttt c Phe Phe <i>I</i> 135			Ğlu	_		_	_		_	_		_	
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Leu Gly N	Met Ile 35	Val	Gly	Ser	Phe 40	Val	Ser	Ile	Ser	Ala 45	Glu	Pro	Pro
Leu Val (	Gly Ile	Phe :	Leu (	Gln 55	Lys	Ser	Ser	Ser	Ser 60	Trp	Pro	Ala	Ile
Glu Gln A	Ala Leu	Val '	Thr (	Gly	Gln	Glu	Leu	Gly 75	Ile	Ser	Ile	Leu	Gly 80
Gly Ala H	His Ala	Asp 1	His '	Val	Arg	Lys	Leu 90	Ser	Gly	Pro	Ser	Asp 95	Gln
Arg Phe 0	Glu Asn 100	Leu	Gly '	Trp	Ala	Ser 105	Thr	Glu	Asn	Gly	Ala 110	Ile	His
Leu Glu (	Gly Ala 115	Asp A	Ala (	Gln	Leu 120	Thr	Thr	Lys	Leu	His 125	Asp	Leu	Gln
Glu Ile 0 130	Gly Asp	His		Phe 135	Ala	Val	Leu	Glu	Val 140	Ile	Asp	Ala	Ser
Ala Asp 0 145	Gln Asp		Ser : 150	Ser	Ala	Leu	Val	Tyr 155	His	Arg	Ser	Gln	Val 160
Ser Ser I	Leu												
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215 220 225 ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta 835 Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu 230 235 240 gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln 250 aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc 931 Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe 265 aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc 979 Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala 280 gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg 1027 Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu 295 gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag 1075 Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu 310 cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac 1121 Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val 330 ttgaaaaatg cac 1134 <210> 704 <211> 337 <212> PRT <213> Corynebacterium glutamicum <400> 704 Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile 40 Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr 105 Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly

115

125

120

Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu 135 Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu 145 150 Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe 215 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu 245 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe 265 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly 310 315 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val <210> 705 <211> 1089 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1066) <223> RXA02741 actggtcacc tggtttggtc tgcactctga ctcccctcaa aagggcacaa tttggtcaat 60 ttcccaacct tgtctttcag tcatggttag tgtgggaacc atg aag gca atc tta Met Lys Ala Ile Leu

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					gat Asp								211
				_	act Thr								259
					ggt Gly 60								307
					gcg Ala								355
_	_		_	_	cag Gln	_		_	 _	 _	_	_	403
		_		 	gtg Val	_	_	_	 _	 _		_	451
_	_				cat His								499
_			_	_	ctc Leu 140			_	 	 	_		547
					gcg Ala								595
					aaa Lys								643
					tcc Ser								691
					gtt Val								739
					tta Leu 220								787
					tcg Ser								835

				cgc cca agc Arg Pro Ser	
		u Gly Glu		cgt gca cag Arg Ala Gln 275	
				cgc gtt act Arg Val Thr 290	
_			-	gac ctt cag Asp Leu Gln 305	
agc acg agc Ser Thr Ser 310		u Val Leu		aag gac taaa Lys Asp	acacgca 1076
taaaaagatc d	ctg				1089
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Glu Val Asp 35	Met Ala Gl	y Val Asn 40	Phe Ile Asp	Thr Tyr Tyr 45	Arg Gln
Gly Glu Tyr 50	His Ala An	g Leu Pro 55	Phe Ile Pro	Gly Phe Glu 60	Gly Thr
Gly Arg Val 65		p Pro Gln ( 0	Gly Leu Ile 75	Ala Ala Gly	Thr Lys 80
Val Ala Trp	Cys Asp Al	a Met Gly	Ser Tyr Ala 90	Gln Gln Val	Cys Val 95
Pro Arg Asp	Arg Leu Va 100		Pro Glu Gly 105	Val Ser Ser 110	Glu Val
Ala Ala Ser 115	Met Leu Me	t Gln Gly 1 120	Ile Thr Ala	His Tyr Leu 125	Thr Asn
Gly Val Tyr 130	Glu Leu Gl	u Glu Gly 7 135	Asp Ser Cys	Leu Ile Thr 140	Ala Gly
Ala Gly Gly 145	Val Gly Le		Thr Gln Met 155	Ala Ala Ala	Lys Gly 160
Val Arg Val	Tyr Ser Va 165	l Val Ser '	Thr Asp Glu 170	Lys Ala Glu	Leu Ala 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala 180 185 Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg 210 215 Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys 265 Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro 315 Lys Asp <210> 707 <211> 990 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(967) <223> RXN02560 <400> 707 ttggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60 ggaacttcta agagcagtgg aatgaaataa teeggtgetg atg eag gge aac teg Met Gln Gly Asn Ser ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro 10 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro 25 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val 40 45

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	agg Arg 55														307
	tcc Ser	-	_		_	-					_	_	-		355
	gtc Val														403
	act Thr	_	_	_		_			 -	-				_	451
	tgg Trp														499
_	ctc Leu 135				_		_		_		-				547
	ctc Leu														595
	ctt Leu		_		-			_	 _		_		_		643
-	gcc Ala				_									_	691
	ggc Gly														739
	cct Pro 215														787
	aaa Lys														835
	tat Tyr														883
	agg Arg														931
	ggc Gly										taaa	aagca	atg		977
att	atgga	acg (	cct												990

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<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr 260 265 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu 275 280 285 Arg

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							aataa				atg		ggc	aac	tcg	115
		_	-	-		_	gag Glu	_	_	_		-	_			163
							tac Tyr									211
	_				_		gat Asp 45	_			_		_		_	259
						_	gtt Val	_	_	_			_			307
							gga Gly					_	_	_		355
							cct Pro									403
							cac His									451
							cga Arg 125									499
							gat Asp									547
							gct Ala		Asn							595

														gat Asp 180		643
_	_				_									cct Pro	_	691
		_	_	_				_	_		-		-	gga Gly		739
			_			-	-		_			_		tac Tyr		787
				_			_			-	_	_		gac Asp		835
			_			_		_			_	_	_	acg Thr 260		883
						cgc Arg	_		_			-				922

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<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp

130		135		140		
Glu Ala Ala 145	Trp Gly Phe 150	Leu Asp Ala	Gly Ile 155	Ala Ala	Gln Asn	Ala 160
Ala Ile Ala	Ala Glu Ser 165	Leu Gly Leu	Gly Thr 170	Leu Tyr	Leu Gly 175	Ser
Val Arg Asn	Asp Ala Glu 180	Ala Val His 185	Lys Leu	Leu Gly	Leu Pro 190	Pro
Glu Ile Val 195	Pro Val Val	Gly Leu Glu 200	Met Gly	His Ala 205	Asp Pro	Pro
Glu Pro Ala 210	Gly Ile Lys	Pro Pro Leu 215	Pro Gln	Glu Ala 220	Ile Val	His
Trp Asp Thr 225	Tyr Thr Glu 230	Lys Asn Leu	Glu Leu 235	Ile Asp	Ser Tyr	Asp 240
Arg Ala Leu	Asp Thr Tyr 245	Tyr Ser Arg	Tyr Gly 250	Gln His	Gln Leu 255	Trp
Ser Lys Gln	Thr Ala His 260	Arg Ala Ala 265	Ser Lys	Arg Cys	Tyr Lys 270	Asn
Gln Glu						
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tcttcgaatc t	gtcccactg ca	agacaagga ac	tacaagta	_	ctt aca Leu Thr	
gag atc tgg Glu Ile Trp						
gtc cag gtt Val Gln Val						
gac cac gta Asp His Val 40						
ttc gcc tct Phe Ala Ser				_		

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	55					60					65					
										aac Asn 80						355
										acc Thr						403
										gac Asp						451
										ggc Gly						499
										cac His						547
							-			atc Ile 160		-		_	_	595
										ctg Leu						643
	-							_		aag Lys			_			691
_	-	_	_	_	-	_	-	_	_	acc Thr					_	739
										ccc Pro						787
acc Thr 230	gct Ala	gtg Val	gca Ala	gct Ala	gtc Val 235	acc Thr	aag Lys	gaa Glu	cgt Arg	gcg Ala 240	cgt Arg	gca Ala	gct Ala	ttc Phe	cga Arg 245	835
		gac Asp		tagt	cttt	aa t	ccaa	agtaa	ng ta	ac						870

<210> 712

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

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Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser

20 25 30 Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His 135 Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile 145 150 155 Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu 170 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys 185 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro 215 Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala 230 235 Arg Ala Ala Phe Arg Gly Lys Asp Asp 245 <210> 713 <211> 929 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(906) <223> RXN03014 <400> 713 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr 10 ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg

48

Leu	Gly	Ala	Ser 20	Pro	Ala	Arg	Val	Arg 25	Ser	Gly	Val	Gly	Tyr 30	Val	Met	
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						ttg Leu 55										192
						act Thr										240
						gct Ala						-				288
_	-					gcg Ala		_	_	_					_	336
	_	_		_		ggt Gly						_	-	_	-	384
						tcc Ser 135					_	-				432
						ggt Gly										480
						ttt Phe		_	-	_					_	528
			-	_		gga Gly		_	_		_					576
						att Ile	_	-	_			_		_		624
_		-		-	-	caa Gln 215	_				_	_	_	_		672
						tcc Ser										720
						ggt Gly										768
_		_			_	gcc Ala		-	_	-		_	_	_		816

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			260					265					270		
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				ggt Gly											
taaa	agac	gcc (	cccga	atgga	ag ca	aa									
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	0> 7: Val		Phe	Glu 5	Val	Leu	Leu	Val	Ala 10	Ser	Tyr	Val	Leu	Leu 15	Thr
Leu	Gly	Ala	Ser 20	Pro	Ala	Arg	Val	Arg 25	Ser	Gly	Val	Gly	Tyr 30	Val	Met
Val	Ser	Met 35	Ala	Ser	Ser	Met	Val 40	Phe	Leu	Phe	Gly	Leu 45	Ala	Met	Val
Tyr	Ala 50	Ser	Val	Gly	Thr	Leu 55	Asn	Met	Ala	His	Val 60	Gly	Leu	Arg	Met
Glu 65	Asp	Val	Pro	Ser	Gly 70	Thr	Arg	Ser	Ala	Ile 75	Phe	Ala	Val	Leu	Leu 80
Val	Ala	Phe	Gly	Ile 85	Lys	Ala	Ala	Val	Phe 90	Pro	Leu	Asp	Ser	Trp 95	Leu
Pro	Asp	Ser	Tyr 100	Pro	Thr	Ala	Pro	Ser 105	Leu	Val	Thr	Ala	Val 110	Phe	Ala
Gly	Leu	Leu 115	Thr	Lys	Val	Gly	Val 120	Tyr	Ser	Ile	Ile	Arg 125	Ala	Arg	Ser
Ile	Ile 130	Phe	Thr	Asp	Gly	Ser 135	Leu	Asp	Thr	Met	Leu 140	Met	Trp	Val	Ala
Leu 145	Ala	Thr	Met	Leu	Ile 150	Gly	Ile	Leu	Gly	Ala 155	Met	Ala	Gln	Asn	Asp 160
Ile	Lys	Arg	Leu	Leu 165	Ser	Phe	Thr	Leu	Val 170	Ser	His	Ile	Gly	Tyr 175	Met
Ile	Phe	Gly	Val 180	Ala	Leu	Gly	Ser	Ala 185	Gln	Gly	Leu	Ser	Gly 190	Ala	Ile
Phe	Tyr	Ala 195	Ile	His	His	Ile	Leu 200	Val	Gln	Thr	Ser	Leu 205	Phe	Leu	Val
Val	Gly 210	Leu	Val	Glu	Arg	Gln 215	Ala	Gly	Ser	Ser	Ser 220	Leu	Arg	Arg	Leu

864

906

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Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly 245 250 Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly Met Gly Pro Tyr Arg Arg Arg Cys His Leu Thr Ala His Leu Val 275 280 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro 295 <210> 715 <211> 1280 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1257) <223> FRXA00910 <400> 715 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc 48 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met 20 gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg 192 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc 240 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg 288 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu 85 90 ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca 336 Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala 100 105 110 384 ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser 115 120 125 att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gta gca 432 Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala

130 135 140 ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat 480 Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp 145 150 155 atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg 528 Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc 576 Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg 624 Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val 195 gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt 672 Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Leu Arg Arg Leu 210 215 gga too ctg gca tat atc too cca ctt ctt gcg att ttg tac ttc atc 720 Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile 225 230 ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc 768 Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly 245 aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca 816 Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala 260 tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac 864 Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr 275 280 acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac 912 Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp 295 qcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat 960 Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg 1008 Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt 1056 Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu 340 345 gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc 1104 Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala 360 gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly 375 370 380

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Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp
385

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag
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405

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Asp Gln Pro

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<400> 716

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Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp 145 150 155 160

Ile Lys Arg Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gl<br/>n Gly Leu Ser Gly Ala Ile 180 \$180\$ 185 \$190\$

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu 210 215 220 Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile 225 230 235 Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala 265 Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp 290 295 Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu 345 Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly 375 Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu 405 Asp Gln Pro <210> 717 <211> 1051 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1051) <223> RXN01895 <400> 717 cgcgtacacg tgctcaacac gacaacgctt aaacggctgc acgcgtaaca cggcagaccg 60 cacaagcttt aagatccacg atcaggagac tttgacaaat atg tca gtt aac cca 115 Met Ser Val Asn Pro acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt 163 Thr Arg Pro Glu Gly Gly Arg His His Val Val Ile Gly Ser Gly 10 15

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				-	_							cag Gln 50		_	_	259
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												gtc Val				355
						_			_			acc Thr	-		_	403
				-	_				_		_	gtc Val	_		_	451
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												cgt Arg				547
												cca Pro				595
gaa Glu	cgc Arg	ctg Leu	ctc Leu	acc Thr 170	ttc Phe	gtc Val	gtt Val	gtt Val	ggc Gly 175	gct Ala	ggc Gly	cca Pro	acc Thr	ggt Gly 180	gtt Val	643
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		_							_	_		atc Ile 210	_		_	739
												cta Leu				787
												cgc Arg				835
												aag Lys				883

ggc gaa gag Gly Glu Glu			Ser									931
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Lys Ala Asp 35	Val Asp	Val Thr	Leu 40	Ile	Asp	Arg	Thr	Asn 45	His	His	Leu	
Phe Gln Pro 50	Leu Leu	Tyr Gln 55		Ala	Thr	Gly	Ile 60	Leu	Ser	Ser	Gly	
Glu Ile Ala 65	Pro Ser	Thr Arg 70	Gln	Ile	Leu	Gly 75	Ser	Gln	Glu	Asn	Val 80	
Asn Val Ile	Lys Gly 85	Glu Val	Thr 2	Asp	Ile 90	Asn	Val	Glu	Ser	Gln 95	Thr	
Val Thr Ala	Ser Leu 100	Gly Glu		Thr 105	Arg	Val	Phe	Glu	Tyr 110	Asp	Ser	
Leu Val Val 115	Gly Ala	Gly Ala	Gly (	Gln	Ser	Tyr	Phe	Gly 125	Asn	Asp	His	
Phe Ala Glu 130	Phe Ala	Pro Gly 135	Met :	Lys	Ser	Ile	Asp 140	Asp	Ala	Leu	Glu	
Ile Arg Ala 145	Arg Ile	Ile Gly 150	Ala	Phe	Glu	Arg 155	Ala	Glu	Ile	Cys	Glu 160	
Asp Pro Ala	Glu Arg 165	Glu Arg	Leu :		Thr 170	Phe	Val	Val	Val	Gly 175	Ala	
Gly Pro Thr	Gly Val 180	Glu Leu		Gly 185	Gln	Leu	Ala	Glu	Met 190	Ala	His	
Arg Thr Leu 195	Ala Gly	Glu Tyr	Lys 2	Asn	Phe	Asn	Thr	Asn 205	Ser	Ala	Lys	

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys 210 215 Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn 235 Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr 245 Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala 275 Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val 310 <210> 719 <211> 816 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(816) <223> FRXA01895 <400> 719 cac cac ctc ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc 48 His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag 96 Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag 144 Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu 40 tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192 Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc 240 Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat 288 Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp 85 90 gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag 336 Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu

105

						gag Glu										384
_		_				ggt Gly 135	_			-		_	_	_		432
						gct Ala										480
	_	_			_	ctt Leu	_		_		_	_				528
						cgc Arg										576
	-		-	_	_	aac Asn	_	_	_			_	_	_		624
						aag Lys 215	-		_					-		672
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His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln 20 25 30

Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu 35 40 45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu 50 55 60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly

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65 70 75 80 Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp 85 Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu 100 105 Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val 120 Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu 130 135 Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro 170 Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met 185 Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys 235 Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val 265

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10 15 20 gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg 211 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu 25 cat gcg ctc cag cat gct gtt ccg aat cgt gcc ctg ctg ccg ttg ctc 259 His Ala Leu Gln His Ala Val Pro Asn Arg Ala Leu Leu Pro Leu Leu 40 acc atg aat aaa cca ggc ggc atc gac tgt cct ggt tgt gct tgg cct 307 Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro Gly Cys Ala Trp Pro 55 gag cct tcc act gcc aac ctt ggt gtg gtt gag ttc tgc gag aac ggt 355 Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu Phe Cys Glu Asn Gly gcc aag gcg gtc gcc gag gaa aca aca cct gat cgt gcc ggc aaa gag 403 Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp Arg Ala Gly Lys Glu ttc tgg gca gag cat tct att tat gat ctg cgg gaa aag acc gat cac 451 Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg Glu Lys Thr Asp His 105 tgg ctg gga aag cgt ggc cga atc acc gag ccc atg ttt tat gat cgt 499 Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro Met Phe Tyr Asp Arg 120 125 tet tet gge gat gat eac tac ege eet att tet tgg gat egt gea ttt 547 Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser Trp Asp Arg Ala Phe 135 gcg atc att gcg tcg aag ctc cgc gag atc gag cca gat gaa gcg gtg 595 Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu Pro Asp Glu Ala Val 155 ttt tac acc tct ggt cga gca ccc aat gag ccg gct tat atg ctg cag Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro Ala Tyr Met Leu Gln 170 ctt cta gcc cgc cga ctt ggc aca aat aat ctt cca gac tgt gga aac 691 Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu Pro Asp Cys Gly Asn atg tgc cac gag tcc acc ggt act qcc ttq ggt gag acc ttq ggt ttq 739 Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly Glu Thr Leu Gly Leu ggc aag gga tcc gtg gtg atg gag gat ttc tac aac act gat ttg ttg 787 Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr Asn Thr Asp Leu Leu 220 att tcc gtg gga caa aac ccg ggc acc aac cac cca cgt gcg ttg acg 835 Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His Pro Arg Ala Leu Thr 235 240 gct ttc aaa gaa ttg aag gaa aac ggt ggc aag att ctg gcg ctg aac Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys Ile Leu Ala Leu Asn 250 255

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						tca Ser										979
						cgc Arg 300										1027
						cta Leu										1075
						atc Ile										1123
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	-		_		_	-		_			ggt Gly 545		_		_	1747
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	_	_				-	_			_	ccg Pro	_		-		1843
	-		-	-	-				_		att Ile					1891
-			_	_		_					ttc Phe					1939
		_									ggc Gly 625	_	_		_	1987
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											cgc Arg					2131
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2409

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Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro 50 55 60

Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu 65 70 75 80

Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp 85 90 95

Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg 100 105 110

Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro 115 120 125

Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser 130 135 140

Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu 145 150 155 160

Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro 165 170 175

Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu 180 185 190

Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly 195 200 205

Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr 210 215 220

Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His 225 230 235 240

Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys 245 250 . 255

Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg 265 Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala 280 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln 295 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val Asn Phe Leu Leu Thr Gly Asn Ile Gly Lys 395 Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser 475 Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr 530 535 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp 550 555 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln

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Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr 585 Ile Pro Gly Phe His Asp Phe Asn Arg Ile Asp Asn Pro Gly Gly 595 600 Phe Leu Leu Pro Asn Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn 615 Gly Lys Ala Gln Leu Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro 625 630 Lys Asp Tyr Leu Leu Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn Ser Thr Ile Tyr Gly Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly Arg Arg Val Val Phe Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu 695 Arg Arg Ala Pro Asn Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp 725 730 Ser Val Ala Glu Lys Ser Asn Thr Pro Val Ser Lys Ser Val Val Val Arg Leu Glu Ala Thr Gly Arg Thr Ala Ser <210> 723 <211> 1038 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1015) <223> RXN00705 <400> 723 gttctggaac aagcactgat gattgggccg agtccacgtt ggttaatgct ctgcatcttc 60 aagaaatcat cgctaaaaat tacccggagg ctaaataaaa atg ggt cgg att acc 115 Met Gly Arg Ile Thr caa aac ttg cag gtc cca cgc gtt gtg tcc act gac gag caa gtt ttt 163 Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe 10 15 gtt aac act cgt ccg gat act gtt gcg gtg gag gag cct cta gaa att 211 Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile

30

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					gat Asp								451
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-	-				gca Ala 140	-	_		 _		_		547
					acg Thr								595
				_	ccg Pro		_	_		-			643
					aag Lys								691
					ggt Gly								739
					ggt Gly 220								787
					gga Gly								835
					tct Ser								883
					atc Ile								931

210

atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg 979 Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg 280 285 290 ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga 1025 Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu Gly 295 300 acaggtagaa cag 1038 <210> 724 <211> 305 <212> PRT <213> Corynebacterium glutamicum <400> 724 Met Gly Arg Ile Thr Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn 105 Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn 135 Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys 185 Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu 200 Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala

215

230

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu

Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val 245 250 Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu 280 Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu 295 Gly 305 <210> 725 <211> 908 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(885) <223> FRXA00705 <400> 725 cca cgc gtt gtg tcc act gac gag caa gtt ttt gtt aac act cgt ccg 48 Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144 Ala Leu Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val 35 cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192 His Gly Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val 50 ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His 100 105 gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu 120 gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432

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Val Ala Ala 130	Gln Arg	Asn Val		Thr	Thr	Ser	Ala 140	Cys	Gly	Val	Cys	
ggc acg acg Gly Thr Thr 145												480
acg ccg att Thr Pro Ile												528
ttg aag tcg Leu Lys Ser		_		_					_		_	576
gct ggt ttg Ala Gly Leu 195					_	_			_		_	624
gtc ggt cgg Val Gly Arg 210			Asp		_				_	_	_	672
gcg gga aag Ala Gly Lys 225												720
gcg tct ttt Ala Ser Phe			_	_	_	_	_			_		768
gta atc gct Val Ile Ala		-		_	_	_					_	816
gat tca ggt Asp Ser Gly 275												864
cac tat gcg His Tyr Ala 290			•	gcca	iga a	cago	gtaga	ia ca	ng			908
<210> 726 <211> 295 <212> PRT <213> Coryno	ebacteri	um gluta	micum	1								
<400> 726	W-1 0	mb - 7	<b>C1</b>	C1	77 - J	DI.	** - 7	7	m)	7	<b>D</b>	
Pro Arg Val 1	val Ser 5	Thr Asp	Glu	GIN	10	Phe	Val	Asn	Thr	Arg 15	Pro	
	Ala Wal	Glu Glu	Pro		Glu	Ile	Arg	Val		Gly	Thr	,
Asp Thr Val	20			25					30			
Asp Thr Val Ala Leu Thr 35	20	Met Arç	Thr 40		Gly	His	Asp	Ile 45		Leu	Val	

Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn 65 70 75 80

Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala 85 90 95

Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His 100 105 110

Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu 115 120 125

Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys 130 135 140

Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile 145 150 155 160

Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys 165 170 175

Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala 180 185 190

Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp 195 200 205

Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met 210 215 220

Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg 225 230 235 240

Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly 245 250 255

Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln 260 265 270

Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn 275 280 285

His Tyr Ala Gly Glu Leu Gly 290 295

<210> 727

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXN00388

<400> 727

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					Met 1	Leu	Pro	Val	Asn 5	
				gcc Ala 15						163
				ctc Leu						211
				caa Gln						259
				gat Asp						307
				gac Asp						355
				caa Gln 95						403
				atg Met		_		_	_	451
				tac Tyr						499
				ctg Leu						547
				atg Met	Ala			Phe		595
				gca Ala 175						643
				tcc Ser						691
				tcc Ser						739
				ggc Gly						787
				gat Asp						835

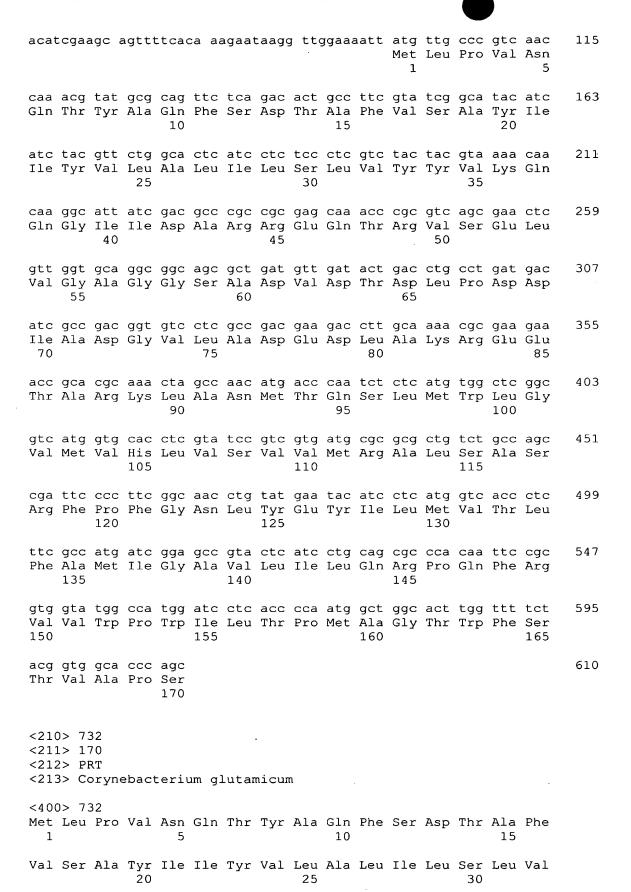
230 235 240 245 gcg atc tgg act gtc cca atc ttc ggc ctg ggc atc atc ttg ggt gcc 883 Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala 255 260 250 atc tgg gca gaa gca gcc tgg ggt cgt ttc tgg gga tgg gat cct aag 931 Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys 265 270 gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac 979 Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His 280 285 gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac 1027 Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn 295 300 1075 atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met 310 315 gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt 1121 Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn 330 tggttggcgg ggt 1134 <210> 728 <211> 337 <212> PRT <213> Corynebacterium glutamicum <400> 728 Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg 105 Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile 115 120 Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln 130 135 140

Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu 155 150 145 Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser 180 185 190 Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu 200 Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe 215 Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn 230 Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly 245 Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp 265 Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn 295 Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu 310 315 Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu 330 325 Asn <210> 729 <211> 326 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(303) <223> FRXA00388

BGI-126CP - 1041 -

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr 40 tgg gtt ctc tac gct ggt tac ctc cac gca cgt gca act gct ggt tgg 192 Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp 55 ege aac ace aac get gea tgg ate aac ate etg geg etg gte aeg atg 240 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met 288 att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser tac gcc gga ctg aac taagcacttt tggttggcgg ggt 326 Tyr Ala Gly Leu Asn 100 <210> 730 <211> 101 <212> PRT <213> Corynebacterium glutamicum <400> 730 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser 90 Tyr Ala Gly Leu Asn 100 <210> 731 <211> 610 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(610) <223> FRXA00386 <400> 731

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BGI-126CP - 1043 -

Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr 35 40 45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr 50 55 60

Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu 65 70 75 80

Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser 85 90 95

Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg 100 105 110

Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile 115 120 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln 130 135 140

Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala 145 150 155 160

Gly Thr Trp Phe Ser Thr Val Ala Pro Ser 165 170

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<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXA00945

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Met Leu Glu Arg Leu

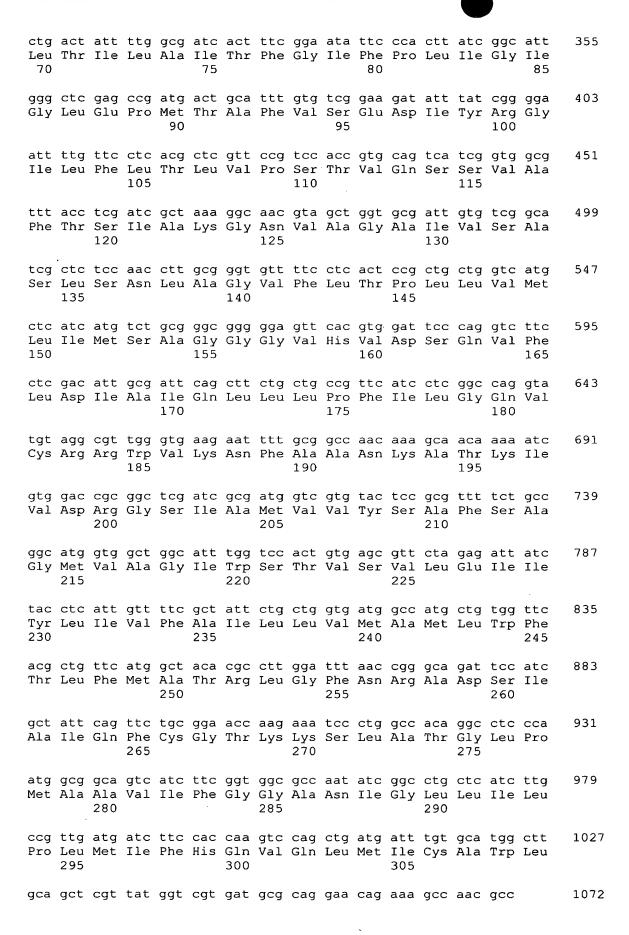
1 5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg 163 Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val 10 15 20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc 211 Ala Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val 25 30 35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc 259
Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg
40 45 50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac 307 Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His 55 60 65







taaaagtcct cagtagctag cca

1095

<210> 734

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

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Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
20 25 30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe 35 40 45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
50 55 60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe 65 70 75 80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu 85 90 95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val. Pro Ser Thr Val 100 105 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly 115 120 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr 130 135 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val 145 150 155 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Pro Phe 165 170 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn 180 185 190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
195 200 205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser 210 215 220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met 225 230 235 240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn 245 250 255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu

0

270 260 265 Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile 280 Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met 290 295 Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala <210> 735 <211> 1281 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1258) <223> RXN02556 <400> 735 tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60 gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115 Leu Ile Val Ser Thr cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val 10 atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr 25 ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala 40 45 aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307 Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp get cet gac cea gtt cag etg etg tee ege att gge cac aag cac gtg 403 Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu 110 ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct

499

Phe	Ala	Ala 120	Ile	Val	Glu	Val	Leu 125	Gly	Ala	Glu	Thr	Val 130	Thr	Ala	Pro	
										atc Ile						547
								_		aac Asn 160	-	-				595
_	_		_	_	_					aag Lys	_	_		_	_	643
acc Thr	gtc Val	tgg Trp	gaa Glu 185	tac Tyr	acc Thr	ctg Leu	gca Ala	ggt Gly 190	gag Glu	ctg Leu	gtt Val	gcc Ala	cca Pro 195	gag Glu	cca Pro	691
										gac Asp						739
_	-	_		_	_					gac Asp				_		787
	-		_			_	_			ttc Phe 240	_		_	_	_	835
	_		_	_		_	_			gcg Ala	-		-	_	-	883
										att Ile						931
			_			-		-		atg Met			-	_	_	979
										tcc Ser						1027
										cct Pro 320						1075
										gag Glu						1123
										ggc Gly						1171
										gag Glu						1219

360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser 375 380 385

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<400> 736

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Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  $$85\ .$  90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala

				245					250					255		
Ala	Gly	Asp	Leu 260	Val	Leu	Asn	Lys	Asp 265	Thr	Asn	Pro	Val	Val 270	Leu	Ile	,
Ser	Gln	Gly 275	Ile	Gly	Ser	Thr	Pro 280	Met	Val	Gly	Met	Leu 285	Ala	Gly	Met	
Asn	Pro 290	Glu	Arg	Asp	Val	Val 295	Val	Leu	His	Ala	Asp 300	Gln	Ala	Glu	Ser	
Thr 305	Tyr	Ala	Gln	Val	Glu. 310	Glu	Val	Gln	Gly	Leu 315	Val	Glu	Lys	Leu	Pro 320	
Lys	Ala	Ala	Phe	Glu 325	Ile	Phe	Tyr	Arg	Asp 330	Asn	Asp	Gln	Trp	Leu 335	Glu	
Val	Ala	Gly	Arg 340	Ile	Pro	Ser	Gly	Ala 345	Ser	Val	Tyr	Leu	Cys 350	Gly	Gly	
Val	Glu	Phe 355	Leu	Lys	Asn	Val	Arg 360	Glu	Gln	Ile	Glu	Ala 365	Leu	Asp	Glu	
Gln	Pro 370	Arg	Asp	Val	Asn	Phe 375	Glu	Leu	Phe	Ala	Pro 380	Asn	Asp	Trp	Leu	
Ile 385	Ser															
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gtag	gaaat	ta q	gecea	atgaa	ag ca	atgga	aaag	g cga	aaaa	cccc	_		_	tcc Ser		115
					cgc Arg											163
					cct Pro											211
					aag Lys											259
					ggc Gly											307

55 60 65 ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp 70 75 gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403 Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val 90 tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu 105 ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro 120 gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547 Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu 135 140 atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595 Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly 150 gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca 643 Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala 170 acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691 Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro 185 190 ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag 739 Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln 200 ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att 787 Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile 215 gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta 835 Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val 235 tee gtt ggt gae aag att gaa gee aee ate geg gee gge gae etg gtt Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val 250 ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc 931 Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly 270 tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac 979 Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp 285 gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg 1027 Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val 300 305

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu 310 315 320 325	1075
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile 330 335 340	1123
cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys 345 350 355	1171
aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val 360 365 370	1219
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Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His 35 40 45	
Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly 50 60	
Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met 65 70 75 80	
Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile 85 90 95	
Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile 100 105 110	
Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu 115 120 125	
Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile 130 135 140	
Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn 145 150 155 160	
Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys	

165 170 175 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu 180 185 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp 200 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe 225 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp Val Val Leu His Ala Asp Gln Ala Glu Ser 295 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu 330 Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly 345 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu 375 Ile Ser 385 <210> 739 <211> 1200 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1177) <223> RXA01392 <400> 739 gtctgcaatc accccgaaca tttgttcaat cgttgatttt cattccactt cgtaatattg 60 ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca Val Ala Asn Thr Ser 1

gat Asp		_	 _				_	_	_				163
cgc Arg	_				_	_	_	_	_	-	_		211
 gga Gly		-		-	_	_	-						259
gag Glu 55													307
cac His													355
tcg Ser													403
gat Asp		_				_		 _	_			-	451
cag Gln													499
gtc Val 135													547
tac Tyr					_					_	_		595
cgt Arg						Tyr		 	_	_			. 643
gcg Ala													691
agg Arg													739
cgg Arg 215													787
cgt Arg													835

				, ,	cgt Arg		_	-	-				_	883
_		-		-	atc Ile		-	_	-			 	_	931
	_			_	acc Thr					_		_		979
_		_	_		tac Tyr									1027
					gga Gly 315									1075
	-	_	_		ggc Gly					_	-	 _	_	1123
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<213> Corynebacterium glutamicum

<400> 740

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Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala 50 60

Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu 65 70 . 75 80

Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp 85 90 95

Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val 100 105 110

Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp

115 120 125 Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys 135 Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu 145 150 155 Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala 170 Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu 185 Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp 280 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala 295 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly 310 315 Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys 345 Asn Pro Glu Pro Phe Gln Lys 355 <210> 741 <211> 1227 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1204) <223> RXA00800 <400> 741

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			_	_	_		aag Lys		-	_	_	-		_		163
							gct Ala									211
_	_			_			gac Asp 45	_	_		_	_		_		259
							ctc Leu									307
							acc Thr									355
							tgc Cys									403
			_		_		aac Asn				_		_	_	_	451
							ctg Leu 125									499
	_	_	_		_	_	cac His	_		_	-		_	-		547
							gct Ala									595
							aac Asn									643
							ggt Gly									691
							tcc Ser 205									739
							aag Lys									787
aat	tcc	tct	ggt	ctt	ggt	ggc	gaa	ggt	gat	gcc	tct	gag	gtc	gtg	gca	835

	•														
Ser	Ser	Gly	Leu	Gly 235	Gly	Glu	Gly	Asp	Ala 240	Ser	Glu	Val	Val	Ala 245	
															883
			_					_					_	-	931
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_				-	_	_			_	_					1075
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								_		taaa	atggo	ctc a	acgad	eggatt	1224
															1227
1> 30 2> PI	58 RT	ebact	eriu	nw dj	Lutan	nicum	α								
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Glu	Lys	Val 20	Asn	Val	Val	Val	Pro 25	Asp	Pro	Gly	Ala	Asn 30	Asp	Val	
Val	Lys 35	Ile	Gln	Ala	Cys	Gly 40	Val	Cys	His	Thr	Asp 45	Leu	Ala	Tyr	
Asp 50	Gly	Asp	Ile	Ser	Asp 55	Glu	Phe	Pro	Tyr	Leu 60	Leu	Gly	His	Glu	
Ala	Gly	Ile	Val	Glu 70	Glu	Val	Gly	Glu	Ser 75	Val	Thr	His	Val	Glu 80	
	gttl Val gtal gtal gcaa Ala gat Asp 295 gca Ala gat Arg ggc Gly 0> 74 Ser Glu Val Asp	gtt cgt Val Arg  gta ggc Val Gly  gca ggc Ala Gly 280  gat gtt Asp 295  gca tgg Ala Trp  gat ctg Asp Leu  cgt att Arg Ile  ggc gac Gly Asp 360  0> 742 1> 368 2> PRT 3> Coryne	gtt cgt gag Val Arg Glu  gta ggc atc Val Gly Ile 265  gca ggc cgc Ala Gly Arg 280  gat gtt cct Asp Val Pro 295  gca tgg tac Ala Trp Tyr  gat ctg cac Asp Leu His  cgt att ggt Arg Ile Gly 345  ggc gac gtg Gly Asp Val 360  0> 742 1> 368 2> PRT 3> Corynebact 0> 742 Ser Thr Val  Glu Lys Val 20  Val Lys Ile 35  Asp Gly Asp 50	gtt cgt gag ctc Val Arg Glu Leu 250  gta ggc atc atg Val Gly Ile Met 265  gca ggc cgc atg Ala Gly Arg Met 280  gat gtt cct gcg Asp Val Pro Ala 295  gca tgg tac ggc Ala Trp Tyr Gly  gat ctg cac ctg Asp Leu His Leu 330  cgt att ggt ctt Arg Ile Gly Leu 345  ggc gac gtg ctg Gly Asp Val Leu 360  0> 742 1> 368 2> PRT 3> Corynebacteriu 0> 742 Ser Thr Val Val 5  Glu Lys Val Asn 20  Val Lys Ile Gln 35  Asp Gly Asp Ile 50	gtt cgt gag ctc acc Val Arg Glu Leu Thr 250  gta ggc atc atg ccg Val Gly Ile Met Pro 265  gca ggc cgc atg gtg Ala Gly Arg Met Val 280  gat gtt cct gcg att Asp Val Pro Ala Ile 295  gca tgg tac ggc gac Ala Trp Tyr Gly Asp 315  gat ctg cac ctg cag Asp Leu His Leu Gln 330  cgt att ggt ctt gat Arg Ile Gly Leu Asp 345  ggc gac gtg ctg cgt Gly Asp Val Leu Arg 360  0> 742 1> 368 2> PRT 3> Corynebacterium gl 0> 742 Ser Thr Val Val Pro 5  Glu Lys Val Asn Val 20  Val Lys Ile Gln Ala 35  Asp Gly Asp Ile Ser 50  Ala Gly Ile Val Glu	gtt cgt gag ctc acc gat Val Arg Glu Leu Thr Asp 250  gta ggc atc atg ccg acc Val Gly Ile Met Pro Thr 265  gca ggc cgc atg gtg atg Ala Gly Arg Met Val Met 280  gat gtt cct gcg att gat Asp Val Pro Ala Ile Asp 295  gat ctg cac ctg cag ggt Asp Leu His Leu Gln Gly 330  cgt att ggt ctt gat gat Arg Ile Gly Asp Asp 345  ggc gac gtg ctg cgt tct Gly Asp Val Leu Arg Ser 360  0> 742 1> 368 2> PRT 3> Corynebacterium glutam 0> 742 Ser Thr Val Val Pro Gly 5  Glu Lys Val Asn Val Val 20  Val Lys Ile Gln Ala Cys 35  Asp Gly Asp Ile Ser Asp 50  Asp Gly Asp Ile Ser Asp 55  Ala Gly Ile Val Glu Glu	gtt cgt gag ctc acc gat ggt Val Arg Glu Leu Thr Asp Gly 250  gta ggc atc atg ccg acc tgg Val Gly 11e Met Pro Thr Trp 265  gca ggc cgc atg gtg atg gat 285 gat gtt cct gcg att gat Val 285  gat gtt Pro Ala Ile Asp Phe 300  gca tgg tac ggc gac tgc ctg Ala Trp Tyr Gly Asp Cys Leu 315  gat ctg cac ctg cag gac tgc ctg Asp Leu His Leu Gln Gly Arg 330  cgt att ggt ctt gat gat gtt Arg Ile Gly Leu Asp Asp Val 345  ggc gac gtg ctt gat gat gtt Arg Ile Gly Leu Arg Ser Val 365  0> 742 1> 368 2> PRT 3> Corynebacterium glutamicum 0> 742 Ser Thr Val Val Pro Gly Ile 5  Glu Lys Val Asn Val Val Val Val Val 20  Val Lys Ile Gln Ala Cys Gly Asp Gly 35  Asp Gly Asp Ile Ser Asp Glu 55  Ala Gly Ile Val Glu Glu Val	gtt cgt gag ctc acc gat ggt ttc Leu Thr Asp Gly Phe 250  gta ggc atc atc acc gat ggt ttc 250  gta ggc atc atc acc cga acc tgg cag Yal Gly Ile Met Pro Thr Trp Gln 270  gca ggc cgc atg gtg atg gtg ggc Ala Gly Arg Met Val Met Val 285  gat gtt cct gcg att gat ttt tac Asp Val Pro Ala Ile Asp Phe Tyr 300  gca tgg tac ggc gac ggc cgg ctg cct Ala Trp Tyr Gly Asp Cys Leu Pro 315  gat ctg cac ctg cag ggt cgg ttc Asp Leu His Leu Gln Gly Arg Phe 330  cgt att ggt ctt gat gat gtt gaa Arg Ile Gly Leu Asp Asp Val Glu 350  ggc gac gtg ctg cgg tct ggt gtg Gly Asp Val Son 365  gc gac gtg ctg cgg tct ggt gtg gtg Son 365  gc gac gtg ctg ctg cgt tct gtg gtg Son 365  gc gac gtg ctg ctg cgt tct gtg gtg Son 365  gc gac gtg ctg ctg cgt tct gtg gtg Son 365  cot att ggt ctg cgt tct gtg gtg Son 365  gc gac gtg ctg ctg cgt tct gtg gtg Son 365  Gly Asp Val Asn Val Val Val Pro Son 365  Corynebacterium glutamicum  0> 742  Ser Thr Val Val Pro Gly Ile Val Son 40  Asp Gly Asp Ile Gln Ala Cys Gly Val 35  Asp Gly Asp Ile Ser Asp Glu Phe 50  Ala Gly Ile Val Glu Glu Val Gly	## STATE   STA	## STATE   STA	## Cat   Gat   ## Cot   Cot	## Company of Company	gta cgt cat gag att gat ttt tac ggt cgc ggt gga tcc gtg Asp Val Pro Ala Ile Asp Cly Fhe Tyr Gly Asp Cys Leu Pro Glu Arg Gly Ett Gas act Ala Trp Tyr Gly Asp Cgt Ala Gly Arg His Leu Gln Gly Arg Phe Pro Thr Tyr Glu Arg Bat ttt cat act Ala Trp Tyr Gly Asp Val Ser Val Ser Ile Gly Asp Val Pro Thr Tyr Gly Arg Bat ttt tac ggt cgc ggt gga tcc gtg Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg	gat cgt cgt gag catc acc gat ggt ttc ggc acc gat gtt tac acc gat gat ccc acc ggac yall gas ggc atc ggc atc ggt ggg atg ggc atc ggc atg ggt ggg atg ggc ggt cat ggg atg ggc atg ggc atg ggg atg ggg ggc ggt yall gas have yall gly val Pro Asn Leu Thr Ser Arg 280  gaa ggc cgc atg gtg atg ggg ggc ggt cca aac ctg acg tct cgc Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg 280  gat ggt cct gcg att gat ttt tac ggt cgc ggt gga tcc gtg cgc Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg 295  gat ggt cct gcg gat ggt ttt tac ggt ggt gga tcc gtg cgc Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg 295  gca tgg tac ggc gac ggt ggt ccc gag cgt ggt ttc cca act tat Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr 325  gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt tct Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser 3350  cgt att ggt ctt gat gat gat gaa gag gct ttc aac acc atg aag Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys 345  ggc gac gtg ctg ctt gtg tgt gag gad atc acc atg aag Arg Ile Gly Arg Ser Val Val Glu Glu Ala Phe Asn Thr Met Lys 365  ggc gac gtg ctg ctg tct gtg gt gad gad atc accacacgacgatt acc yall yall yall Glu Ile Ser Thr Val Val Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro 15  Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val 306  Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu 50  Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu 50  Ala Gly Ile Val Glu Glu Glu Val Gly Glu Ser Val Thr His Val Glu	

Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys 85 90 95

Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn 100 Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln 130 135 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Gly Leu Leu 150 155 Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp 165 Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala 225 Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg 295 Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu 330 Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala

Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile

<sup>&</sup>lt;210> 743

<sup>&</sup>lt;211> 1011

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Corynebacterium glutamicum

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			aaa ccc tct gct aag aag 1 Lys Pro Ser Ala Lys Lys 20	163
			gtc gca ggt gca ttg gct 2 Val Ala Gly Ala Leu Ala 35	211
			etc gca acc gcg atc act 2 Leu Ala Thr Ala Ile Thr 50	259
	-		gac gat cag gca ctt atc 3 Asp Asp Gln Ala Leu Ile 65	307
			gc atc acc tgc cac ggc 3 Cys Ile Thr Cys His Gly 80 85	355
_			ect tee ete gta ggt gtt 4 Pro Ser Leu Val Gly Val 100	403
		-	cc ggc cgt atg cca ata 4 Ser Gly Arg Met Pro Ile 115	451
			gct cct cgt tac acc gag 4 Ala Pro Arg Tyr Thr Glu 130	499
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		Asp Gly Thr I	etc gcc atg gag gag ctc 5 Leu Ala Met Glu Glu Leu .60 165	595
			cc gcc gac gtc gct cgc 6 Ger Ala Asp Val Ala Arg 180	643
			cc tgc cac aac ttc act 6 Ger Cys His Asn Phe Thr 195	691
ggt cgt ggt ggc	gca ctg tcc	tct ggt aag t	ac gca cca aac ctg gat 7	739

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BGI-126CP - 1060 -

Gly Arg Gly 200	Gly Ala	Leu Ser	Ser 205	Gly	Lys	Tyr	Ala	Pro 210	Asn	Leu	Asp	
gct gca aac Ala Ala Asn 215		_		_	_	_					-	787
aac atg cct Asn Met Pro 230							-	-		_	_	835
gac atc atc Asp Ile Ile				Thr								883
ggt tac tca Gly Tyr Ser												931
tgg gta ttc Trp Val Phe 280					_	-	_	_				979
tca cgt tca Ser Arg Ser 295	tgagtaac	aa caac	gacaa	a ca	g							1011
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<pre>&lt;211&gt; 296 &lt;212&gt; PRT &lt;213&gt; Coryne &lt;400&gt; 744 Met Met Glu     1  Pro Ser Ala  Ala Gly Ala     35  Ala Thr Ala     50  Asp Gln Ala     65  Ile Thr Cys  Ser Leu Val</pre>	Thr Asn 5  Lys Lys 20  Leu Ala  Ile Thr  Leu Ile  His Gly 85	Pro Gln  Val Lys  Leu Thr  Pro Asp 55  Ser Glu 70  Val Asn	Thr Asn Ile 40 Ala Gly Leu Gly	Pro Arg 25 Gly Gln Lys	10 Arg Leu Val Asp Gly 90	Lys Ser Ala Leu 75 Val	Val Gly Thr 60 Tyr	Arg Ala 45 Ala Asp	Arg 30 Gly Gln Val	15 Thr Ile Arg Ala Gly 95	Val Leu Asp Cys 80 Pro	
<pre>&lt;211&gt; 296 &lt;212&gt; PRT &lt;213&gt; Coryne &lt;400&gt; 744 Met Met Glu     1  Pro Ser Ala  Ala Gly Ala     35  Ala Thr Ala     50  Asp Gln Ala     65  Ile Thr Cys  Ser Leu Val</pre>	Thr Asn 5 Lys Lys 20 Leu Ala Ile Thr Leu Ile His Gly 85 Gly Val 100	Pro Gln  Val Lys  Leu Thr  Pro Asp 55  Ser Glu 70  Val Asn  Gly Glu	Thr Asn Ile 40 Ala Gly Leu Gly	Arg 25 Gly Gln Lys Gln Ala 105	10 Arg Leu Val Asp Gly 90 Val	Lys Ser Ala Leu 75 Val	Val Gly Thr 60 Tyr Glu Phe	Arg Ala 45 Ala Asp Asp	Arg 30 Gly Gln Val Arg Val 110	15 Thr Ile Arg Ala Gly 95 His	Val Leu Asp Cys 80 Pro	

Ala Asn Gly Gly Gro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu 155 Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser 165 170 Ala Asp Val Ala Arg Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser 185 Cys His Asn Phe Thr Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr 195 200 Ala Pro Asn Leu Asp Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met 215 Leu Thr Gly Pro Gln Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser 225 Ala Asp Glu Lys Lys Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu 250 Thr Pro Ser Pro Gly Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala 280 Ala Met Trp Ile Gly Ser Arg Ser <210> 745 <211> 502 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(502) <223> RXN03096 <400> 745 aagatcatgc tcatcgaagc cggcgcccga agatggcagt tggctggcat gggtccttat 60 egeaggegee gttgteacet eactgeteac ettgtaeace atg gtt etg gte tgg 115 Met Val Leu Val Trp tee aag gee tte tgg ege gae egt aaa gae gee eee gat gga gea aee 163 Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr 10 gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc 211 Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc 259 Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe 45 50 too act goo ctg ttg gtt too goa too ctt got gta too gtg oto goa 307

Ser	Thr 55	Ala	Leu	Leu	Val	Ser 60	Ala	Ser	Leu	Ala	Val 65	Ser	Val	Leu	Ala	
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_				_	_	-	_		ggc Gly 95				_			403
	-		_	_		_	_	_	acg Thr				-			451
			_			-	_		agg Arg					_		499
att Ile																502

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<400> 746

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Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro

Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala 50 55 60

Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala 65 70 75 80

Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro 85 90 95

Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro 100 105 110

Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr 115 120 125

Asn His Asp Gln Trp Ile 130

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gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser 25 30 35
acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala 40 45 50
ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val 55 60 65
cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe 70 75 80 85
gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe 90 95 100
ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys 105 110 115
gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501 Val Arg Glu Arg Ala Ala Gly Leu Ser Asn 120 125
ttt 504
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Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala 50 55 60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala 65 70 75 80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile 85 90 95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
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Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn 115 120 125

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<223> RXN02765

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Met Ser Asn Gln Leu

1 5

ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa 163 Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu 10 15 . 20

caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg 211 Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val

ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc 259 Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr 40 45 50

cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc 307 Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg

tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc 355 Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe 70 80 85

tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt 403 Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly 90 95 100

ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg 451

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Leu	Arg	Leu	Ala 105	Asp	Ala	Leu	Val	Asp 110	Thr	His	Ala	Pro	Glu 115	Pro	Val	
_					_	_	_		cag Gln	-		_		_		499
									att Ile							547
			-		_			_	ctg Leu					_		595
					-				ctg Leu 175	_	_					643
	-	_			-	_		_	ctg Leu	_			_	_		691
		_				_		_	ccg Pro	-			_	_	_	739
									ttg Leu							787
									aac Asn							835
	tcg Ser							tgaç	ggtat	gt o	eggaa	ataca	aa ad	cc		882
	)> 75															
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<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

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Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
20 25 30

Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly 35 40 45

Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val 50 55 60

Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp 65 70 75 80

Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His 100 105 Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala 120 Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn 130 135 Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu 185 Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln 215 Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg 225 230 235 Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile 245 <210> 751 <211> 1059 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1036) <223> RXN02206 <400> 751 ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccqtact 60 accttatgac ctcagtagtg tggtgggcgt gaaacagcga atg gtc ggt tca agt Met Val Gly Ser Ser ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163 Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211 Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn 25 30 35 tet ggt gge acg ett ate gae gte tee eee aac tae ace ace gge gte 259 Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val

40 45 50 gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307 Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser 55 gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc Ala Val Val Ile Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu 70 ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp 90 gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451 Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499 Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu 120 gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547 Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly 135 tat tee ggt tgg cag tta geg gte ace cae get gea tee aat eat gea 595 Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala 150 gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643 Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu 170 ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691 Leu Glu Arg Arg Ala Glu Gln Glu Leu Pro Ala Thr Gln His Leu 185 ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739 Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr 200 gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787 Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr 215 220 gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro gct gtc aca gcc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931 Ala Val Thr Ala Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys 280 285

gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat 1027 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp 300 gtc tcc ctg tgacttggtc caattacatt cac 1059 Val Ser Leu 310 <210> 752 <211> 312 <212> PRT <213> Corynebacterium glutamicum <400> 752 Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Asn Leu Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu 105 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr 135 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala 155 Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro 180

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly 200

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser 210

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp 235

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly 245 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg 260 265 270 Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu 280 Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr 290 295 Gln Ala Leu Asp Asp Val Ser Leu 310 <210> 753 <211> 747 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(724) <223> RXN02554 <400> 753 gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60 ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag 115 Met Ser His Thr Lys cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163 Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala 10 agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211 Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly 25 259 get gtg gac aaa atc get ett acc get gag atc ett atg eec gge geg Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala 40 45 gtt cca age act get gae cag get gta aag gat gea gat att gtg tte 307 Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355 Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu 70 75 gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403 Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn 90 95 100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att

Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile

110

105

451

115

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att gcg ga Ile Ala Gl 12	. Phe Phe					_		_					499
att ggt ta Ile Gly Ty 135		Ile											547
gcg tat gc Ala Tyr Al 150											-		595
att aag ag Ile Lys Se		Phe							_	_	_		643
ggc cgt at Gly Arg Il													691
aaa gat to Lys Asp Se 20	Arg Leu	_		_		_		tagt	acct	cg a	atcti	cagee	744
aac													747
<210> 754 <211> 208 <212> PRT <213> Corynebacterium glutamicum													
1210, 0017.	iepacteri	um gi	ucam	ııcun	ı								
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_		Pro				Ile 10	Leu	Gly	Ala	Gly	Arg 15	Val	
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<pre>&lt;400&gt; 754 Met Ser Hi 1  Gly Ser Se  Val Ala Gl 3  Leu Met Pr 50  Ala Asp Il 65</pre>	S Thr Lys 5 Leu Ala 20 7 Ser Gly 5 6 Gly Ala 8 Val Phe 8 Thr Leu 85	Pro Arg Ala Val Leu 70 Glu	Ser Val Pro 55 Ala	Ile Ala Asp 40 Ser Val	Ala Val 25 Lys Thr Pro	10 Ala Ile Ala Leu Val 90	Ala Ala Asp His 75	Gly Leu Gln 60 Lys	Tyr Thr 45 Ala Phe	Glu 30 Ala Val Arg	15 Val Glu Lys Ser Asn 95	Lys Ile Asp Val 80	
<pre>&lt;400&gt; 754 Met Ser Hi 1 Gly Ser Se  Val Ala Gl 3 Leu Met Pr 50 Ala Asp Il 65 Asn Pro Ala </pre>	S Thr Lys  Leu Ala 20  Ser Gly  Gly Ala  Val Phe A Thr Leu 85  Val Asn 100  Glu Ile	Pro Arg Ala Val Leu 70 Glu	Ser Val Pro 55 Ala Gly Glu Ala	Ile Ala Asp 40 Ser Val Lys Leu	Ala Val 25 Lys Thr Pro Ile Glu 105	10 Ala Ile Ala Leu Val 90 Glu	Ala Ala Asp His 75 Ile	Gly Leu Gln 60 Lys Asp	Tyr  Thr  45  Ala  Phe  Thr	Glu 30 Ala Val Arg Met	15 Val Glu Lys Ser Asn 95 Pro	Lys Ile Asp Val 80 His	
<pre>&lt;400&gt; 754 Met Ser Hi. 1 Gly Ser Se  Val Ala Gl; 3 Leu Met Pro 50 Ala Asp Ile 65 Asn Pro Ala  Trp Val Pro Ser Thr Se</pre>	S Thr Lys  C Leu Ala  20  7 Ser Gly  6 Gly Ala  2 Val Phe  A Thr Leu  85  9 Val Asn  100  6 Glu Ile	Pro Arg Ala Val Leu 70 Glu Gly Ile	Ser Val Pro 55 Ala Gly Glu Ala	Ile Ala Asp 40 Ser Val Lys Leu Glu 120	Ala Val 25 Lys Thr Pro Ile Glu 105 Phe	10 Ala Ile Ala Leu Val 90 Glu Phe	Ala Ala Asp His 75 Ile Ile Ala	Gly Leu Gln 60 Lys Asp Asp	Tyr Thr 45 Ala Phe Thr Gln Ser 125	Glu 30 Ala Val Arg Met Asp 110	15 Val Glu Lys Ser Asn 95 Pro	Lys Ile Asp Val 80 His Arg	

145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe 185

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg 205

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Thr I		Ile 120	Pro	Gly	Leu	Asn	Ile 125	Ser	Ser	Asn	Ser	Arg 130	Ile	Ala	Phe	
cca a Pro I			_		-	-								_		547
tct as Ser Ly 150																595
ccg a		_			_			_	-		_					643
ttc to					_			-		-	-	_	_	-	-	691
gcc aa Ala A	.sn			-					_	-	_				-	739
acg aa Thr A						_						_	_			787
gta ac Val Tl 230			_	_	_	_			_	_					_	835
atc to				-				-	_	-	-	-	-			883
gag c						-			taga	atgaa	aaa a	aggto	egeta	at		930
taa																933
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Gly H	is	Val	Thr 20	Asp	Ser	Gly	Glu	Val 25	Val	Asn	Met	Leu	Phe 30	Thr	Asp	
Phe A	la .	Asn 35	Gly	Trp	Phe	Ala	Met 40	Asp	Arg	Ile	Val	Leu 45	Ile	Arg	Leu	
Leu Me	et ' 50	Thr	Ala	Val	Val	Val 55	Val	Phe	Phe	Leu	Trp 60	Ala	Met	Arg	Lys	

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu

65					70					75					80	
Asp	Phe	Val	Gly	Ile 85	His	Ile	Ala	Glu	Asp 90	Ile	Leu	Gly	Lys	Lys 95	Lys	
Gly	Arg	Arg	Phe 100	Leu	Pro	Ile	Leu	Ala 105	Thr	Ile	Phe	Phe	Ala 110	Ala	Leu	
Leu	Met	Asn 115	Leu	Ala	Thr	Ile	Ile 120	Pro	Gly	Leu	Asn	Ile 125	Ser	Ser	Asn	
Ser	Arg 130	Ile	Ala	Phe	Pro	Ile 135	Val	Met	Ala	Val	Ala 140	Gly	Tyr	Ile	Ala	
Phe 145	Ile	Tyr	Ala	Gly	Ser 150	Lys	Arg	Tyr	Gly	Phe 155	Phe	Lys	Tyr	Val	Lys 160	
Ser	Ser	Val	Val	Ile 165	Pro	Asn	Ile	Pro	Pro 170	Ala	Leu	His	Val	Leu 175	Val	
Val	Pro	Ile	Glu 180	Phe	Phe	Ser	Thr	Phe 185	Ile	Leu	Arg	Pro	Val 190	Thr	Leu	
Ala	Leu	Arg 195	Leu	Met	Ala	Asn	Phe 200	Leu	Ala	Gly	His	Ile 205	Ile	Leu	Val	
Leu	Leu 210	Phe	Ser	Ala	Thr	Asn 215	Phe	Phe	Phe	Phe	Gln 220	Phe	Asn	Gly	Trp	
Thr 225	Ala	Met	Ser	Gly	Val 230	Thr	Ile	Leu	Met	Ala 235	Val	Leu	Phe	Thr	Val 240	
Tyr	Glu	Ile	Ile	Val 245	Ile	Phe	Leu	Gln	Ala 250	Tyr	Ile	Phe	Ala	Leu 255	Leu	
Val	Ala	Val	Tyr 260	Ile	Glu	Leu	Ser	Leu 265	His	Ala	Asp	Ser	His 270			
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ccga	acao	egg g	gagag	gaaco	gc to	gagco	jttad	c aad	cacto	jtcc	_	aag Lys		-		115
						aaa Lys										163
agt	ggt	gaa	gtc	gtg	aac	atg	ctg	ttc	acc	gat	ttc	gct	aat	ggt	tgg	211

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Ser	Gly	Glu	Val 25	Val	Asn	Met	Leu	Phe 30	Thr	Asp	Phe	Ala	Asn 35	Gly	Trp	
	_	_	_	_		_	ttg Leu 45		_			_	_	_	_	259
_		_					gct Ala	_	-	_		_		-	_	307
		_	_			_	gag Glu		-		_		_			355
		_	_	_			gga Gly	_	_			_			_	403
							ttc Phe									451
_			_				atc Ile 125					_		_		499
							ggt Gly									547
							aaa Lys									595
							cac His									643
							cca Pro									691
-				-			atc Ile 205		_	-	_				_	739
_						_	ttc Phe					-	_			787
_			_	_	-	-	ctc Leu		_	_					_	835
							ttc Phe									862

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<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu 35 40 45

Leu Met Thr Ala Val Val Val Phe Phe Leu Trp Ala Met Arg Lys 50 55 60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu 65 70 75 80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys 85 90 95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu  $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$ 

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn 115 120 125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala 130  $$135\$ 

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys 145 150 155 160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val 165 170 175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu 180 185 190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val 195 200 205

Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Gln Phe Asn Gly Trp 210 215 220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val 225 230 235 240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala 245 250

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<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

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- 1076 -

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							agc Ser									163
							gag Glu									211
							tcg Ser 45									259
							ggc Gly									307
							gtg Val									355
					-	_	cgt Arg				_	_				403
							cgc Arg							_		451
							gca Ala 125									499
	_	-					gag Glu	-	_		_				_	547
							gat Asp									595
							gac Asp									643
							cag Gln									691
							atc Ile 205									739

						aag Lys									787
-					_	gca Ala				-	-	_			835
						ggc Gly									883
						gtc Val									931
				-		tcc Ser 285		-	-		-		-		979
						gtc Val									1027
			-	_		gat Asp	-								1075
_	_					aag Lys	_		_	_		_			1123
						acc Thr	_		_	_					1171
						cgc Arg 365									1219
						gct Ala									1267
-			_	_	_	ctg Leu	_	_		-	-	_	-	_	1315
						ttg Leu									1363
						cag Gln									1411
						atc Ile 445									1459

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	-		_		-		_	_	gat Asp	_	_	-				1507
									gct Ala							1555
	_			_	_			_	gag Glu 495		_	_		_		1603
_	_		_	_		_	_	_	ttc Phe				_			1651
									gca Ala							1699
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Met 1	Ala	GIU	Leu	Thr.	ile	ser	ser	Asp	Glu 10	TIE	Arg	Ser	Ата	11e 15	Ala	
Asn	Tyr	Thr	Ser 20	Ser	Tyr	Ser	Ala	Glu 25	Ala	Ser	Arg	Glu	Glu 30	Val	Gly	
Val	Val	Ile 35	Ser	Ala	Ala	Asp	Gly 40	Ile	Ala	Gln	Val	Ser 45	Gly	Leu	Pro	
Ser	Val 50	Met	Ala	Asn	Glu	Leu 55	Leu	Glu	Phe	Pro	Gly 60	Gly	Val	Ile	Gly	
Val 65	Ala	Gln	Asn	Leu	Glu 70	Ala	Asp	Arg	Val	Gly 75	Val	Val	Val	Leu	Gly 80	
Asn	Tyr	Glu	Leu	Leu 85	Lys	Glu	Gly	Asp	Gln 90	Val	Arg	Arg	Thr	Gly 95	Asp	
Val	Leu	Ser	Ile 100	Pro	Val	Gly	Glu	Ala 105	Phe	Leu	Gly	Arg	Val 110	Ile	Asn	
Pro	Leu	Gly 115	Gln	Pro	Ile	Asp	Gly 120	Leu	Gly	Glu	Ile	Ala 125	Ser	Glu	Glu	
Asp	Arg 130	Val	Leu	Glu	Leu	Gln 135	Ala	Pro	Thr	Val	Leu 140	Glu	Arg	Gln	Pro	
Val	Glu	Glu	Pro	Leu	Ala	Thr	Gly	Ile	Lys	Ala	Ile	Asp	Ala	Met	Thr	

145 150 155 160 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr 170 Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn 180 185 Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly 315 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp 325 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln 345 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala 410 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile 420 425 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu 440 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val 450 455 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala 470 475

Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser 485 Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu 515 Asp Ala Gly Gln Val Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val 535 Ser Lys Lys 545 <210> 761 <211> 1572 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1549) <223> RXN01193 <400> 761 gtgtggccaa ccaggcacgt caggcacaga tcacccagga aatcacagag attgttggtg 60 gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt 115 Met Thr Thr Ala Leu gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg 10 gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro 25 gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys 40 aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala 75 gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val 90 95 aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser 105 110

						gag Glu 125							499
						ggt Gly							547
						acc Thr							595
						gtg Val							643
_		_		_	_	gag Glu						-	691
	-	 	_		_	gag Glu 205		_			_	_	739
						gac Asp							787
			-	-		atg Met	_	 _	_		 _		835
						gtt Val							883
						acc Thr							931
						gcc Ala 285							979
						gag Glu							1027
						gtt Val							1075
						ttc Phe							1123
						aag Lys				-			1171

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Leu Thr Ser 360	acc tct Thr Ser									1219
cac tac gag His Tyr Glu 375			Val Il							1267
gaa ctt cag Glu Leu Gln 390	-	_		Gly I د					_	1315
gag gac aag Glu Asp Lys										1363
ggt cag aac Gly Gln Asn				s Phe '						1411
tac gtg cca Tyr Val Pro 440										1459
ggc gac ttc Gly Asp Phe 455			Glu Gl							1507
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		_								1572
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Leu Asp Asp Val Ser Leu Asn Asn Pro Glu Ile Glu Arg Trp Gly 115 120 Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu 135 Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val 145 150 155 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr 280 Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr 295 Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro 310 315 Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu 330 Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr 345 Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met 385 390 395 Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg 405 410 Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr

425

Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe 435 440 440 Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe

450 455 46

Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu 465 470 475 480

Thr Gly Lys

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Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn
15 20 25

atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt 146
Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly
30 35 40

cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg 194
Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met
45 50 55 60

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tet etg cag gee gtt tae gtt eet gee gat gae tae ace gae eeg get 290 Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala

cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc 338
Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg

tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc 386 Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser 110 115

acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag 434
Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu
125 130 135 140

gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag gaa ctt cag 482

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Val	Ser	Gln	Arg	Val 145	Ile	Gly	Ile	Leu	Gln 150	Lys	Asn	Lys	Glu	Leu 155	Gln
					ctt Leu										
					gcg Ala										
					aag Lys										
_		-		_	gac Asp 210	_			_		_			_	
					cag Gln										
					aag Lys						taaq	ggtag	gag a	acaca	atggct
gaa															
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1	*******	, ,	7114	5	501	Oly	Leu	1111	10	7114	oru	- y -	1110	15	nop
Val	Gln	Asn	Gln 20	Asp	Val	Leu	Leu	Phe 25	Ile	Asp	Asn	Ile	Phe 30	Arg	Phe
Thr	Gln	Ala 35	Gly	Ser	Glu	Val	Ser 40	Thr	Leu	Leu	Gly	Arg 45	Met	Pro	Ser
Ala	Val 50	Gly	Tyr	Gln	Pro	Thr 55	Leu	Ala	Asp	Glu	Met 60	Gly	Val	Leu	Gln
Glu 65	Arg	Ile	Thr	Ser	Thr 70	Lys	Gly	Arg	Ser	Ile 75	Thr	Ser	Leu	Gln	Ala 80
Val	Tyr	Val	Pro	Ala 85	Asp	Asp	Tyr	Thr	Asp 90	Pro	Ala	Pro	Ala	Thr 95	Thr
Phe	Ala	His	Leu 100	Asp	Ala	Thr	Thr	Glu 105	Leu	Asp	Arg	Ser	Ile 110	Ala	Ser
Lys	Gly	Ile 115	Tyr	Pro	Ala	Val	Asn 120	Pro	Leu	Thr	Ser	Thr 125	Ser	Arg	Ile
Leu	Glu	Pro	Ala	Ile	Val	Gly	Glu	Arg	His	Tyr	Glu	Val	Ser	Gln	Arg

130 135 140 Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala 150 155 Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala 165 170 Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala 185 Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr 195 Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala 225 Tyr Lys Lys Leu Thr Gly Lys 245 <210> 765 <211> 739 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(739) <223> FRXA01203 <400> 765 gtgtggccaa ccaggcacgt caggcacaga tcacccagga aatcacagag attgttggtg 60 gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt 115 Met Thr Thr Ala Leu gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg 10 gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys 40 45 aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile 55 60 cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala 70 75 80

_		_		_	_		att Ile		_				_	_	_	403
							ttg Leu									451
_							gag Glu 125						_			499
			_	_			ggt Gly	_				_	_			547
	_	_		_			acc Thr			-	_			_		595
							gtg Val									643
-			_		_	_	gag Glu								_	691
							gag Glu 205									739
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Arg	Gly	Glu 35	Leu	Pro	Ala	Leu	Tyr 40	Asn	Ala	Leu	Thr	Val 45	Glu	Val	Thr	
Leu	Glu 50	Ser	Val	Lys	Lys	Thr 55	Val	Val	Leu	Glu	Val 60	Ala	Gln	His	Leu	

Gly Arg Val Val Lys Lys Thr Jle Ala Met Ala Pro Thr Asp Gly Asp Val Glu Phe Pro Solution Arg Gly Asp Val Lys Lys Thr Jle Ala Met Ala Pro Thr Asp Gly Asp Asp Val Asp Gly Ala Ala Ala Ala Nal Arg Gly Asp Val Val Lys Gly His Val Asp Asp Asp Val Gly Asp Val Val Asp Asp Organization Arg Gly Asp Val Val Asp Gly His Val Asp Asp Organization Asp Val Asp Organization Asp

		115					120					125				
Ile	His 130	Arg	Glu	Pro	Pro	Ser 135	Phe	Asp	Gln	Leu	Glu 140	Gly	Lys	Thr	Glu	
Ile 145	Leu	Glu	Thr	Gly	Ile 150	Lys	Val	Ile	Asp	Leu 155	Leu	Thr	Pro	Tyr	Val 160	
Lys	Gly	Gly	Lys	Ile 165	Gly	Leu	Phe	Gly	Gly 170	Ala	Gly	Val	Gly	Lys 175	Thr	
Val	Leu	Ile	Gln 180	Glu	Met	Ile	Thr	Arg 185	Ile	Ala	Arg	Glu	Phe 190	Ser	Gly	
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cago	ccga	aac a	acaco	gggca	ac ca	agaaa	aggga	a acq	gacad	cctc	_			atc Ile		115
					acc Thr											163
					acc Thr											211
					gag Glu											259
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					gtt Val 75						taat	cago	cta a	actta	accga	360
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Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
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                                                                   115
                                             Val Gly Tyr Gly Ile
gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct
Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc
                                                                   211
Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc
                                                                   259
Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
                             45
ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag
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Leu Val Ala Gly Phe Leu Phe
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<400> 770

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Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala
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Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
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Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
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ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile 50 55 60

ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln 65 70 75 80

gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys 85 90 95

gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro 100 105 110

gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala 115 120 125

gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432

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	cgt Arg		_	_								_				528
	atg Met															576
	aaa Lys			_	_		_	_		_	taaa	agaca	acg a	acgaa	attaga	629
caa																632
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1	Cys	Leu	Arg	1rp 5	гуѕ	ser	GIU	Pro	10	vaı	Leu	GIU	vai	15	ьys	
Asp	Ala	Ala	Glu 20	Gln	Thr	Trp	Ser	Thr 25	Pro	Arg	Glu	Phe	Arg 30	Ala	Gly	
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Gly	Gln 50	Leu	Gly	Gln	Val	Glu 55	Asp	Glu	Leu	Phe	Arg 60	Leu	Ser	Arg	Ile	
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Glu	Ile	Gly	Gly	Arg 85	Arg	Asp	Leu	Leu	Ala 90	Lys	Val	Leu	Tyr	Gly 95	Lys	
Val	Thr	Ala	Val 100	Thr	Glu	Ala	Leu	Ala 105	Leu	Gln	Ala	Ile	Gly 110	Arg	Pro	
Glu	His	Asn 115	Pro	Ile	Asp	Asp	Ile 120	Ala	Ala	Leu	Ala	Gly 125	Ala	Val	Ala	
Glu	Leu 130	Gln	Gly	Arg	Ser	Val 135	Ala	His	Val	Val	Thr 140	Ala	Val	Glu	Leu	
Asn 145	Glu	Gly	Gln	Gln	Gln 150	Ala	Leu	Ala	Glu	Lys 155	Leu	Gly	Arg	Ile	Tyr 160	
Gly	Arg	Ala	Met	Ser 165	Ile	His	Ser	Glu	Val 170	Asp	Thr	Ser	Leu	Leu 175	Gly	

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Val Glu Leu Val Ser Val Glu Arg Met Leu Trp Ala Gly Gln Ala Ser
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Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile Gly Val Leu Pro Asp
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His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn Gly Val Val Thr Ile
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Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly Val Ser Asp Gly Phe
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Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu Ala Asp Phe Ala Val
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Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala Gly Leu Arg Ala Val
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cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc

Arg 70	Glu	Ġly	Gly	Lys	Arg 75	Ala	Ala	Val	Leu	Val 80	Val	Thr	Ser	Asp	Arg 85	
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							att Ile	_				-	_		_	595
							gga Gly									643
							cac His									691
							gtg Val 205				-		-			739
							gaa Glu									787
	Gly	Glu	Val	Glu	Pro	Asp	tac Tyr	Glu	Phe	Glu	Pro	Asp	Ala	Asp		835
							cag Gln									883
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Met Arg Thr Phe Ala

1 5

get tat att gec att gat ggc etc age ttt tec tae eec aac acc cae  $\,$  163 Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His  $\,$  10  $\,$  15  $\,$  20

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ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc  $\phantom{0}$  259 Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile  $\phantom{0}$  40  $\phantom{0}$  50

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acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
70 75 80 85

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gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct 499 Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala

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					_	-	cgc Arg	_		_	_	-		_	_	643
_	_			_	_	_	att Ile		_	_						691
							ctc Leu 205									739
			_		_	_	cac His	_	_				_		-	787
_					_		gat Asp		_							835
		_	-	-			gcc Ala									883
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							cca Pro		Glu							1171
							gaa Glu 365								_	1219

gtg g Val G	-						_					-			_	1267
cac a His I 390																1315
agc g Ser V																1363
ccc g Pro G	-		_		_		_	_		_	_	_	_		_	1411
gaa a Glu I	_	_	-				_	_	-	_		_	_		_	1459
aaa g Lys G		_							-	_		_	-			1507
acg t Thr S 470	_		_	-	_			_		-				_		1555
cgc g Arg V																1603
ctt g Leu A																1651
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Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro 65 70 75 80

Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val 85 90 95

Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp 100 105 110

Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp 115 120 125

Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala 130 135 140

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Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Phe Ala 165 170 175

Leu Ala Ala Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu 180 185 190

Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu 195 200 205

Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe 210 215 220

Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu 225 230 235 240

Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe 245 250 255

Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr 260 265 270

Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu 275 280 285

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Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys 325 330 335

Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe 340 345 350

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										tat Tyr						307
		_	_		_					gaa Glu 80		_		_		355
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		-						-	_	att Ile						451
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										atg Met						787
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ctg	ctt	ttt	gcg	ggg	cac	gaa	aca	acc	acc	acg	ttg	atc	tcc	aat	tgt	931

BGI-126CP - 1102 -

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Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr 55 60

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